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OM nucleic - nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Total number of hits satisfying chosen parameters:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Perfect score:
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                                                                                                                                                                                                                                  Result
  00000
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                                                                                                                                                                                                                                                                                                                  Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
                                                                                                                                                                                                             Score
                 38.65
38.65
34.26
33.24
33.26
33.27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        November 6, 2002, 14:03:45; Search time 32.7914 Seconds (without alignments) 10995.308 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N_Geneseq_032802:*

! /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1980.DAT:*

2: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1981.DAT:*

3: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1982.DAT:*

3: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1983.DAT:*

5: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1984.DAT:*

5: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1984.DAT:*

6: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1985.DAT:*

7: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1985.DAT:*

8: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1988.DAT:*

9: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1988.DAT:*

9: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1988.DAT:*

9: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1988.DAT:*
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-833-740-7_COPY_1_210
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  29.6
18.4
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15.8
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15.8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GenCore version 5.1.3 Copyright (c) 1993 - 2002 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                            SIDSI/gcgdata/genesed/geneseqn-embl/NA199.DAT:

SIDSI/gcgdata/genesed/geneseqn-embl/NA109.DAT:

SIDSI/gcgdata/genesed/geneseqn-embl/NA2000.DAT:

SIDSI/gcgdata/genesed/geneseqn-embl/NA2001.DAT:

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SIDSI/gcgdata/genesed/geneseqn-embl/NA2001.DAT:

SIDSI/gcgdata/genesed/geneseqn-embl/NA2001.DAT:
                                                                                                      1612
13327
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AAH43758
AAH04015
AAH15417
AAL07185
AAL07185
AAI60795
AAI59009
ABA83074
AAK94639
                                                                                                                                                                                                                                                                              SUMMARIES
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Human reproductive
Human reproductive
Human polynucleoti
Human polynucleoti
Human transcriptio
Human full-length
                                                                                                                                                                                                                  Description
                                                                                                                               Human cDNA clone (
                                                                                                                                                                       5' flanking and 5'
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29.8	9	9	9	30													30.8			31	32.2	32.4	32.4	32.4	32.4	32.	32.4	32.4	32.4	32.4	32.4	33.2	33.2	33.2	33.2
14.2	14.2		14.2				14.5			14.6	14.7	14.7	14.7	14.7	14.7	14.7	14.7	•	•	•	•	•						15.4	15.4	15.4				15.8	
16489	7958	670	394	11713	11711	2073	980	977	10529	4136	16595	4264	4264	4264	4264	4264	4264	555	555	35414	9370	7632	4345	3464	3346	1285	1276	1194	1194	555	553	11360	11360	7601	7601
22	21	20	22	22	22	22	21	21	19	21	20	22	22	22	22	22	22	22	22	21	22	23	23	22	23	21	23	21	20	22	21	22	22	22	22
æ	AAZ34835	AAV87950	ABA08267	ABA18963	ABA18962	AAL04589	AAC35669	AAC48603	AAV09028	AAZ60231	AAX23521	AAK69248	AAK69247	AAK68504	AAK68503	AAS27636	AAS27635	AAK56984	AAS27072	AAD00147	AAL07075	ABL21136	ABL05570	AAK94358	ABL05802	AAA94846	ABL05803	AAA72250	AAZ41329	AAK92773	AAA94801	AAL04727	AAL03820	AAL36533	AAL36532
DNA encoding novel	Mouse integrin sub	EST CLONE FHLSE.	urm	Human nervous syst	sys	Human reproductive	Arabidopsis thalia	Arabidopsis thatia	tluory	`	Human kidney amino	Human immune/haema	Human immune/haema	Human immune/haema	Human immune/haema	⊃	DNA encoding novel	Human immune/haema	cDNA encoding nove	TR12 related DNA-1	reprodu	Drosophila melanog			Drosophila melanog				ດນ	Human cDNA 3'-end		0	Human reproductive	Human musculoskele	Human musculoskele

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## ALIGNMENTS

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RESULT 1
AAH43758
5' flanking region; 5' UTR; untranslated region; murine; glucagon-like peptide-2; GLP-2; receptor; regulator; intestinal epithelium; lateral hypothalamus; promoter; d
                                                                                                                                                                                                                                               5' flanking and 5' UTR of GLP-2 receptor gene
                                                                                                                                                                                                                                                                    30-JAN-2002 (first entry)
                                                                                                                                                                                                                                                                                          AAH43758;
                                                                                                                                                                                                                                                                                                               AAH43758 standard; DNA; 2170 BP
                                                                                                                                                                                 Mus musculus.
                                                                                                                   misc_RNA
                                                                                                                                                  misc_RNA
           25-OCT-2001.
                               WO200179290-A2
                                                                                                                                                  Location/Qualifiers 1656
                                                                                                                   /note= "Punitive transcriptional start site"
1761..1763
                                                                        /note= "Corresponds to translational start in rat/human
GLP-2R gene"
1875..1877
                                                      /note= "Putative translational start site"
                                                                                                          /*tag=
                                                                                                                                         /*tag=
                                                                                                                                                                                                         promoter; ds
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AAH04015/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This sequence represents the 5' flanking and 5' UTR of the murine CC glucagon-like peptide-2 (GLP-2) receptor gene. This sequence may be used in the DNA construct of the invention, such that it is linked CC used in the DNA construct of the invention, such that it is linked CC for expression with a heterologous gene of interest. This construct CI is useful for screening compounds to identify regulators of GLP-2 CC receptor expression. The DNA construct is also useful for delivering CC a gene product to tissues selected from intestinal epithelium and the CC lateral hypothalamus, by transfecting an organism, or a gametic or CC cembryonic form of such an organism, with the construct. The DNA CC construct is also useful to identify cells capable of mediating CC expression from the chosen GLP-2R promoter, to identify regions of CC the GLP-2R promoter that are functional in a given cell type, and CC construct agents that modulate expression from the GLP-2R promoter. CC It can be used to map functional regions of the GLP-2R promoter. CC It can be used to map functional regions of the GLP-2R promoter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches 141;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local (
07-FEE-2001
                                  EP1074617-A2
                                                                                                        Human; primer;
                                                                                                                                        Human cDNA clone (5'-primer) SEQ ID NO:850.
                                                                                                                                                                                26-JUN-2001
                                                                                                                                                                                                                    AAH04015;
                                                                                                                                                                                                                                                    AAH04015 standard;
                                                                                                                                                                                                                                                                                                                                              1637
                                                                                                                                                                                                                                                                                                                                                                                                                      1587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1536 TAGGTCTGGGAAAAATCTCCCCAAGATTTTAGGAGGGGCAGGCGGGGGATGA----- 1586
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1476 GTCTTGCTTTTTTTCTTGGGCTTGCTGAGGAAGTCCCCAGGCAGCGTAGACGTCTTGGGGG 1535
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2170 BP; 574 A; 501 C; 550 G; 540 T; 5 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel recombinant DNA construct, useful as drug screening tool and protein delivery vehicle, comprising glucagon-like peptide-2 recept gene, and linked to heterologous gene of interest for expression
                                                                                                                                                                                                                                                                                                                                                           182 GCGTGGAGAGGATTTGTGCAAACATTTCC 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (ONEO-) 1149336 ONTARIO INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-FEB-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3 GCCTTGTTCTTCTCCTCAGCCTGTCAAGGAAGTCCCAGAAAGCACAGCTGACTT-AGGG 61
                                                                                                                                                                                                                                                                                                                                            GCCTGAAGAGGACTTGTGCAAACACTTCC 1665
                                                                                                                                                                                                                                                                                                                                                                                                          -----GAAACTTGGAGATTCGGTAGATCGCTGTAGAGCAACTCAGACAGTC----GGCG 1636
                                                                                                                                                                                                                                                                                                                                                                                                                                           GAGAAGGAACTCTGAAGACTCCGTAGATTGCTCTAGACCGCCTCAGACACTCTCGGCGCA 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                            (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2000US-196909P.
2001US-265310P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2001WO-IB00619
                                                                                            detection; dlagnosis; antisense therapy; gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  29.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 62.2; DB 24;
Pred No. 1.3e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 2170;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20;
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AAH15417/c
                                                RESULT 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention describes primer sets for synthesising 5602 (C full-length cDNAs defined in the specification. Where a primer set CC comprises: (a) an oligo-dT primer and an oligonucleotide complementary ct to the complementary strand of a polynucleotide which comprises one of C the 5602 nucleotide sequences defined in the specification, where the CC oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprises at least 15 nucleotides; or (b) a combination of complementary strand of a polynucleotide which comprises a 5'-end complementary to a complementary and the complementary to a co
                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
  AAH15417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29-JUL-1999;
27-AUG-1999;
11-JAN-2000;
02-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 772 BP; 147 A; 258 C; 194 G; 170 T; 3 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs
                                                                                                                        138
                                                                                                                                                              157 GACCGCCTCAGACACTCTCGGCGCAGCGTGGAGAGGATTTGTGCA 201
                                                                                                                                                                                                                       198
                                                                                                                                                                                                                                                                                                                      258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; SEQ ID 850; 2537pp + CD ROM; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2001-318749/34.
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                                                                                                                                                                                                                                                                     97
                                                                                                                                                                                                                                                                                                                                                                      37
                                                                                                                                                                                                                                                                                                                                                                                                                                              Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            the present invention.
                                                                                                                   CACCTCATAGGGAAGACAGGCCTGATCCTGGTGAGGGTTTGCCCA
                                                                                                                                                                                                                                                                                                                                                          TAAATCTGGAGGAAGCTCTTGCCTGGGGGAACATTACAGAGCCTGGAGCATAGGTTA 139
                                                                                                                                                                                                                                                           CAGGGGCGGGGGATGAGCCAGGGCCGAGAAGGAACTCTGAAGACTCCGTAGATTGCTCTA 156
                                                                                                                                                                                                                                                                                                              CCCAAGAAGCACAGGACCACCTGGGAAAGACAGGGGACAGTCTCCCAGCCTGGGCACCCT 199
                                                                                                                                                                                                                                                                                                                                                                                                                     86;
                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
standard; cDNA; 1612 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HELIX RES INST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Isogai T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sugiyama T,
                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; 2000JP-0118776.
; 2000JP-0183767.
; 2000JP-0241899.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99JP-0300253
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nishikawa T,
                                                                                                                                                                                                                                                                                                                                                                                                                                 18.4%;
52.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hikawa T, Hayashi K, Saito K, Y
Wakamatsu A, Nagai K, Otsuki T;
                                                                                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 38.6; DB Pred. No. 0.023;
                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 772;
                                                                                                                                                                                                                                                                                                                                                                                                          Indels
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AAH15417; 26-JUN-2001

(first entry)

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; primer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             07-FEB-2001.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29-JUL-1999;
27-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28-JUL-2000; 2000EP-0116126.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  09-JUN-2000; 2000JP-0241899
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11-JAN-2000;
02-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dT primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the the 5602 nucleotide comprises at least 15 nucleotides; or (b) a combination oligonucleotide comprises at least 15 nucleotides; or (b) a combination
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (HELI-) HELIX RES INST.
                                                                                                                                                                                                                                                                                                                                                                                                          the specification. The primers sets can be used in antisense therapy and in gene therapy. The primers are useful for synthesising polynucleotides, in gene therapy. The primers are useful for synthesising polynucleotides, in gene therapy. The primers are useful for synthesising polynucleotides, particularly full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs easily without any specialised methods. AAH03166 to AAH13628 and cDNAs easily without any specialised methods. AAH03166 to AAH13628 and AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to AAH13633 represent human amino acid sequences; and AAH13629 to AAH13632 AAB95893 represent human amino acid sequences; and AAH13628 to AAH13632 AAB95893 represent oligonucleotides, all of which are used in the exemplification represent oligonucleotides, all of which are used in the exemplification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end sequence and an oligonucleotide comprising a sequence complementary to a sequence and an oligonucleotide comprises a 3'-end sequence, where the polynucleotide which comprises a 1 least 15 nucleotides and the combination of oligonucleotide comprises at least 15 nucleotides and the combination of the 5'-end sequence is selected from those defined in the 5'-end sequence is selected from those defined in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 8; SEQ ID 13627; 2537pp + CD ROM; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2001-318749/34.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               full-length cDNAs -
                                                                                                                                                                                                                                                                                                                                                  Sequence 1612 BP; 352 A; 476 C; 391 G; 393 T; 0 other;
258 CCCAAGAAGCACAGGACCACCTGGGAAAGACAGGGGACAGTCTCCCAGCCTGGGCACCCT 199
                                          157 GACCGCCTCAGACACTCTCGGCGCAGCGTGGAGAGGATTTGTGCA 201
                                                                                                                                                                                                                 37 CCCAGAAAGCACAGCTGACTTAGGGAAGGTCTGGGAAAAATCTCCCTGCTTTTTGGGGGGG 96
                                                                                                                              97 CAGGGGCGGGGATGAGCCAGGGCCGAGAAGGAACTCTGAAGACTCCGTAGATTGCTCTA 156
                                                                                                                                                                                                                                                                                       Local
                                                                                                                                                                                                                                                                                                                                                                                               the present invention.
                                                                                      TAAATCTGGAGGAAGGAAGCTCTTGCCTGGGGGAACATTACAGAGCCTGGAGCATAGGTTA 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Isogai T,
                                                                                                                                                                                                                                                                  86;
                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sugiyama T, Wakamatsu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99JP-0300253.
2000JP-0118776.
2000JP-0183767.
                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            detection; diagnosis; antisense therapy; gene therapy; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99ЈР-0248036.
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                                                                                                                                                                                                                                                                                            18.4%; 52.1%;

 Mismatches

                                                                                                                                                                                                                                                                                            Score 38.6; DB 22; Length 1612; Pred. No. 0.029;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hayashi K, S
1 A, Nagai K,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Otsuki T;
                                                                                                                                                                                                                                                                                79; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Yamamoto J;
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RESULT 4
AAL02939
AAL02939;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      cancer; gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; reproductive system related antigen; reproductive system disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human reproductive system related antigen DNA SEQ ID NO: 5627.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21-NOV-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                         WO200155320-A2
                                                                                                                                                                                                                                                                                                                                                              04-FEB-2000;
24-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                              31-JAN-2000;
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                                                                                                                                                                                                                                                                                                            07-JUN-2000;
28-JUN-2000;
                                                                                                                                                                                                                                                                                                                                         16-MAR-2000;
17-MAR-2000;
                                                                                             22-AUG-2000;
23-AUG-2000;
30-AUG-2000;
01-SEP-2000;
01-SEP-2000;
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                                                                                                                                                                                                                                                                                                                                  18-APR-2000;
                    05-SEP-2000;
06-SEP-2000;
06-SEP-2000;
08-SEP-2000;
08-SEP-2000;
08-SEP-2000;
08-SEP-2000;
                                                                        01-SEP-2000;
01-SEP-2000;
05-SEP-2000;
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14-AUG-2000;
                                                                                                                                                                                                                                                         26-JUL-2000;
                                                                                                                                                                       14-AUG-2
                                                                                                                                                 18-AUG-2000;
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2000US-0209467.
2000US-0214886.
2000US-0215135.
2000US-0216647.
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2000US-0184664.
2000US-0186350.
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2000US-0224519.
2000US-0225213.
2000US-0225214.
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2000US-0190076.
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                                    2000US-0231242.
2000US-0231243.
                                                                                                                                                                          2000US-0225757.
                                                                                   2000US-0229345
                                                                                                        2000US-0229287
                                                                                                                             2000US-0226868.
2000US-0227182.
               2000US-0231413.
2000US-0231414.
                                                                          2000US-0229509
                                                            2000US-0230437
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AAL07185/c
ID AAL07185 standard; DNA; 496 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
            31-JAN-2000;
04-FEB-2000;
04-FEB-2000;
02-MAR-2000;
16-MAR-2000;
17-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
     18-APR-2000;
                                                                                          17-JAN-2001; 2001WO-US01339
                                                                                                                    02-AUG-2001.
                                                                                                                                         WO200155320-A2
                                                                                                                                                                Homo sapiens.
                                                                                                                                                                                     Human; reproductive system related antigen; reproductive system disorder;
                                                                                                                                                                                                              Human reproductive system related antigen DNA SEQ ID NO: 9873.
                                                                                                                                                                                                                                            21-NOV-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                             AAL07185;
                                                                                                                                                                                                                                                                                                                                                                                      5824 TCATCAGAAGGACAAAGAAGCCAGGGAAACCTGGGGAGATGGGGAGAGGACCCAGGAAGAA 5883
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention provides the protein and coding sequences of a number of human reproductive system related antigens. These can be used in the prevention and treatment of reproductive system disorders, including cancer. The present sequence is a genomic sequence encoding a protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-DEC-2000;
05-DEC-2000;
05-DEC-2000;
05-DEC-2000;
06-DEC-2000;
08-DEC-2000;
08-DEC-2000;
08-DEC-2000;
08-DEC-2000;
08-DEC-2000;
08-DEC-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 13327 BP; 3096 A; 3875 C; 3799 G; 2557 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; SEQ ID NO 5627; 1297pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Isolated nucleic acid molecule encoding a reproductive system antigen is used in preventing, treating or ameliorating a medical condition
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2001-465570/50.
                                                                                                                                                                                                                                                                                                                                                            76 ATCTCCCTGCTTTTGGGGGGGGGGGGGGGGGGGGATGAGCCAGG 118
                                                                                                                                                                                                                                                                                                                                                                                                      16 TCCTCAGCCTGTCAAGGAAGTCCCAGAAAGCACAGCTGACTTAGGGAAGGTCTGGGAAAA 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rosen CA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   05-JAN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local
                                                                                                                                                                                                                                                                                                                                                                                                                                               60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
; 2000US-0179065.
2000US-0180628
2000US-0184664
2000US-018459
2000US-0186350
2000US-0190874
2000US-0190876
2000US-0198123.
                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Barash SC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2000US-0250391
2000US-0251030
2000US-0251989
2000US-0251479
2000US-0251479
2000US-0251856
2000US-0251869
2000US-0251989
2000US-0251989
2000US-0251989
2000US-0251989
2000US-0251989
2000US-0254097
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2001US-0259678
                                                                                                                                                                                                                                                                                                                                                                                                                                                   16.3%; Score 34.2;
58.3%; Pred. No. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ruben SM;
                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 22; Length 13327;
                                                                                                                                                                                                                                                                                                                                                                                                                                       43; Indels
                                                                                                                                                                                                                                                                                                                                               5926
                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
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2000US-0241826 2000US-0244617 2000US-0246474 2000US-0246475 2000US-0246475 2000US-0246477

2000US-0241787. 2000US-0241808. 2000US-0241809.

02-OCT 2000 02-OCT 2000 02-OCT 2000 02-OCT 2000 13-OCT 2000 13-OCT 2000 20-OCT 2000

2000US-0237037 2000US-0237038 2000US-0237039 2000US-0237040 2000US-0239035 2000US-0239935 2000US-0239935 2000US-0240960 2000US-0241221 2000US-0241786 14 - SEP - 2000 21 - SEP - 2000 21 - SEP - 2000 25 - SEP - 2000 25 - SEP - 2000 26 - SEP - 2000 27 - SEP - 2000 27 - SEP - 2000

2000US-0231968 2000US-0232397 2000US-0232399 2000US-0232400 2000US-0232401 2000US-0233063 2000US-0233064 2000US-0233063 2000US-0233063 2000US-0234274 2000US-0234998 2000US-0234998 2000US-0234998 2000US-0235484 2000US-0235484 2000US-0235836

29-SEP-2000; 29-SEP-2000; 29-SEP-2000; 29-SEP-2000; 29-SEP-2000;

2000US-0236327 2000US-0236367 2000US-0236368 2000US-0236369 2000US-0236370 2000US-0236802

08-NOV-2000 01-NOV-2000 01-NOV-2000 01-NOV-2000 01-NOV-2000 01-NOV-2000 01-NOV-2000 01-NOV-2000 01-NOV-2000 01-NOV-2000 01-NOV-2000

2000US-0246524 2000US-0246524 2000US-0246525 2000US-0246526 2000US-0246526 2000US-0246527

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17-NOV-2000; 17-NOV-2000; 17-NOV-2000;

2000US-0249244 2000US-0249245 2000US-0249264 2000US-0249265 2000US-0249297 2000US-0249299 2000US-0249299 2000US-0249309

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2000US-0249216. 2000US-0249217.

2000US-0249218

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19-MAY-2000)
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28-JUN-2000)
30-JUN-2000)
70-JUL-2000)
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11-JUL-2000)
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15-SEP-2000)
23-AUG-2000)
21-SEP-2000]
01-SEP-2000]
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27-SEP-2000;

29-SEP-2000;

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20-CCT-2000;
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2000US-0209467.
2000US-0214886.
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2000US -0217487

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2000US -0218290

2000US -022963

2000US -0224518

2000US -0224518

2000US -0225213

2000US -0225213

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2000US -0236870.
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2000US -0236886.
2000US -0237039.
2000US -0237039.
2000US -0237039.
2000US -0239935.
2000US -0239935.
2000US -0239935.
2000US -0239935.
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2000US-0226868.
2000US-0227182.
2000US-0227009.
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               20-OCT-2000;
20-OCT-2000;
20-OCT-2000;
20-OCT-2000;
20-OCT-2000;
20-OCT-2000;
20-OCT-2000;
20-OCT-2000;
01-NOV-2000;
08-NOV-2000;
17-NOV-2000;
17-NO
           The present invention provides the protein and coding sequences of a number of human reproductive system related antigens. These can be use in the prevention and treatment of reproductive system disorders, including cancer. The present sequence is a genomic sequence encoding protein of the invention.
                                                                                                                                                                                                                                                                                                                                        (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                    Isolated nucleic acid molecule encoding a reproductive system antigen is used in preventing, treating or ameliorating a medical condition
                                                                                                                                                                                                                                                                                                    Rosen
                                                                                                                                                  Disclosure;
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2000US-0241785.
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2000US-0241787.
2000US-0241808.
2000US-0241809.
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2000US-0241826.
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2000US - 0249214.
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2000US-0250160.
2000US-0250160.
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2000US-0251869.
2000US-0251869.
2000US-0251989.
2000US-0251989.
2000US-0251989.
2000US-0254097.
2000US-0254097.
                                                                                                                                               SEQ ID NO
                                                                                                                                                    9873; 1297pp + Sequence Listing;
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                                                                                                                                                           English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous
                                                                                                                                                                                         Wang J,
Zhao QA,
                                                                                Claim 1; SEQ ID NO 4784; 10078pp; English.
                                                                                                                            Novel
                                                                                                                                                                                                                                         (HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                                                14-SEP-2000;
19-OCT-2000;
                                                                                                                                                                                                                                                                                                                                09-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                               26-DEC-2000; 2000WO-US34263
                                                                                                                                                                                                                                                                                                                                                                                                                                   W0200153312-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; nootropic; immunosuppressant; cytostatic; gene therapy; cance, peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
                                                                                                                                                                                                                                                                                                                   19-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human polynucleotide SEQ ID NO 4784.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAI60795 standard; cDNA; 1302 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  leukaemia; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 496 BP; 69 A; 219 C; 108 G; 100 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         141 AAGCCAGTGCCATGAGTTTCGCGCACA 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  179 GCAGCGTGGAGAGGATTTGTGCAAACA 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        261 GGGGAGATCAGGGAGACTGGAGACTACGCTGTTTGGTCCAGGCATAGGAGATGAGCCCTG 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               POCHT
                                                                                                                                                               2001-442253/47
                                                                                                                   nucleic acids and polypeptides, useful for treating disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GCCGGGAAGGGACAGTGTGGATGGGCCAGGCGGAATCAGAGGGTTTCAGAGAAAGCCGTC 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GCCGAGAAGGAACTCTGAAGACTCCGTAGATTGCTCTAGACCGCCTCAGACACTCTCGGC 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Wang Z,
Zhou P,
                                                                                                         central nervous system injuries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                         2000US-0552317
2000US-0598042
2000US-0620312
2000US-0653450
2000US-0662191
2000US-0662193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                  2000US-0727344
                                                                                                                                                                                                                                                                                                                                                       2000US-0488725
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                                                                                                                                                                                   Asundi V, Ch
Wehrman T, X
, Goodrich R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15.9%;
51.7%;
                                                                                                                                                                                               Chen R, Ma Y,
Xu C, Xue AJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 33.4; DB Pred. No. 0.85;
                                                                                                                                                                                      Drmanac RT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 22; Length 496;
                                                                                                                                                                                              Qian XB,
Yang Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            71; Indels
                                                                                                                                                                                             Zhang J;
                                                                                                                                                                                                           Ren F,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                         Wang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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Best Local
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                                                                                                                                                                                         09-JUL-2000;
19-JUL-2000;
03-AUG-2000;
                                               P-PSDB;
                                                         WPI; 2001-442253/47.
                                                                                   Zhao QA,
                                                                                                                                 (HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                                                                                                                                  Human; nootropic; immunosuppressant; cytostatic; gene therapy; cance peripheral nervous system; neuropathy; central nervous system; CNS; Alzhelmer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; Chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
                                                                                                                                                        29-NOV-2000;
                                                                                                                                                                                14-SEP-2000;
                                                                                                                                                                                                                              25-APR-2000;
                                                                                                                                                                                                                                         21-JAN-2000;
                                                                                                                                                                      L9-OCT-2000;
                                                                                                                                                                                                                                                                 26-DEC-2000;
                                                                                                                                                                                                                                                                                           26-JUL-2001
                                                                                                                                                                                                                                                                                                                  WO200153312-A1
                                                                                                                                                                                                                                                                                                                                      Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                    Human; nootropic; immunosuppressant; cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                               Human polynucleotide SEQ ID NO 1212.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAI59009 standard; cDNA; 1732 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              system, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathies and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, Activinyinhibin activity, chemotractic/chemokinetic activity, haemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and
                                                                                                                                                                                                                                                                                                                                                                leukaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22-OCT-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C.N.S disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1302 BP; 275 A; 418 C; 357 G; 252 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          736 GCCGGGAAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        119 GCCGAGAAGG 128
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                                               AAM39853
                                                                               Wang Z,
Zhou P,
                                                                                                                                                                                                                                                                                                                                                                SS
                                                                                                                                                                                         2000US-0552317
2000US-0598042
2000US-0620312
2000US-0653450
                                                                                                                                                                  2000US-0662191
2000US-0693036
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                                                                                                                                                                                                                                                                  2000WO-US34263.
                                                                                                                                                        2000US-0727344
                                                                                                                                                                                                                                         2000US-0488725
                                                                                        Asundi V, Chen R, Ma
Wehrman T, Xu C, Xue
                                                                                Goodrich R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15.8%;
67.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 33.2; Di
Pred. No. 1.3;
                                                                               Drmanac RT;
                                                                                         Ma Y,
Xue AJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB
                                                                                         Qian XB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23;
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                                                                                                   Ren F,
                                                                                         Ç
                                                                                                 Wang
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PS X PP PI I P P PI I P PI I P PI I P P PI I P PI I P PI I
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathies and central nervous system diseases, such as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, activiny, chemotactic/chemokinetic activity, haemostatic activiny, activity, chemotactic/chemokinetic activity, drug screening, and thrombolytic activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and assays for receptor activity, arthritis and inflammation,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; SEQ ID NO 1212; 10078pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       specification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; transcription factor; TRFX; cell proliferative disease; autoimmune disease; inflammation; neurological disease; chromosome 13; developmental disorder; cancer; AIDS; infection; cytostatic; anti-HIV; neuroprotective; antiinflammatory; gene therapy; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human transcription factor TRFX-101 coding sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABA83074;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             05-FEB-2002 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  119 GCCGAGAAGG 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (INCY-) INCYTE GENOMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                             13-MAR-2000; 2000US-0188986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13-MAR-2001; 2001WO-US08117.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       04-OCT-2001
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                                                       Novel transcription factor polypeptides, used to treat diseases associated with altered activity and expression of TRFX, and to for agents capable of modulating its activity -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    59 GGGAAGGTCTGGGAAAAATCTCCCTGCTTTTGGGGGGGCAGGGGCGGGGGGATGAGCCAGG 118
                                                                                                                                                                                                                                                                                                                                           Hillman JL,
                                                                                                                                                                                 P-PSDB; ABB50250.
                                                                                                                                                                                                                                                                            Reddy R;
                                                                                                                                                                                                                                                                                                             Azimzai Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GCCGGGAAGG 727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The sequence data for this patent did not form part of the printed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         47;
                                                                                                                                                                                                                     2001-570896/64.
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                                                                                                                                                                                                                                                                                                                Baughn MR,
Bandman O,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15.8%;
                                                                                                                                                                                                                                                                                                                    Tang
                                                                                                                                                                                                                                                                                                                                                 Yue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No. 1.4;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 33.2;
                                                                                                                                                                                                                                                                                                                       YT,
                                                                                                                                                                                                                                                                                                                                                 Lal P,
                                                                                                                                                                                                                                                                                                                       Mathur
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 22;
                                                                                                                                                                                                                                                                                                                       Lu DAM,
P, Shah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23; Indels
                                                                                                                                                                                                                                                                                                                          DAM, Patterson C;
Shah P, Au-Young
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 1732;
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                                                                                                                      to screen
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Claim 11; Pages 322-323; 327pp; English.

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X S S S S S S S S S S S S S S S S X X
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         including: farteriosclerosis, cirrhosis, hepatitis, cancers, AIDS, allergies, anaemia, asthma, autoimmune thyroiditis, bronchitis, atopic dermatitis, diabetes mellitus, emphysema, Goodpasture's syndrome, gout, Grave's disease, multiple sclerosis, osteoarthitis, pancreatitis, pancreatitis, renumatoid arthritis, systemic lupus erythematosus, ulcerative psoriasis, rheumatoid arthritis, systemic lupus erythematosus, ulcerative psoriasis, rheumatoid arthritis, systemic lupus erythematosus, parkinson's colitis, uveitis, Alzheimer's disease, Huntington's disease, Parkinson's disease, stroke, and viral, bacterial, fungal and protozoal infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present sequence is the coding sequence for a human transcription factor. The transcription factor and its coding sequence are useful in the diagnosis, treatment and prevention of diseases associated with altered expression of the transcription factor e.g. cell proliferative,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   autoimmune/inflammatory, neurological and developmental disorders. A number of specific disorders/diseases are given in the specification,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1801 BP; 387 A; 553 C; 474 G; 387 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; full length cDNA; cDNA synthesis; oligo-capping; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human full-length cDNA, SEQ ID NO: 3613.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               06-NOV-2001 (first entry)
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11-JAN-2000; 2000JP-0118774
02-MAY-2000; 2000JP-0183765
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       801 GCCGGGAAGG 792
The invention relates to primers for synthesising full length cDNA clones. 830 cDNA molecules encoding a human protein have been isolated and nucleotide sequences of 5'- and 3'-ends of the cDNA molecules have been determined. Primers for synthesising the full length cDNA are useful for clarifying the function of the protein encoded by
                                                                                                                                                                                                                                                                                                (HELI-) HELIX RES INST.
                                                                                                                                                                                                                                                                                                                                                                                                    07-JUL-2000; 2000EP-0114089
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 8; SEQ ID NO 3613; 1380pp + sequence listing; English
                                                                                                                                                       830 primers useful for synthesizing full length cDNA clones and their
                                                                                                                                                                                                               WPI; 2001-524255/58.
                                                                                                                                                                                                                                                Wakamatsu A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Match 15.8%;
Local Similarity 67.1%;
                                                                                                                                                                                            p-PSDB; AAM93696
                                                                                                                                        use in genetic manipulation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               47;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                  Sugiyama T,
                                                                                                                                                                                                                                                                                                                                                                      99JP-0194486
                                                                                                                                                                                                                                                    Isogai T, Ha
a T, Nagai K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
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pred. No. 1.5;
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K, Kojima S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 22;
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                                                                                                                                                                                                                                                                            Ishii S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 1801;
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AAL36532
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26 - JUL - 2000;
26 - JUL - 2000;
14 - AUG - 2000;
14 - AUG - 2000;
14 - AUG - 2000;
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Best Local
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30-JUN-2000;
07-JUL-2000;
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24-FEB-2000;
02-MAR-2000;
                                                                                                                                                                                                            07-JUL-2000;
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17-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                          31-JAN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                 17-JAN-2001; 2001WO-US01338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cytostatic: immunosuppressive; nootropic; neuroprotective; antiviral; antiallergic; hepatotropic; antidiabetic; antiinflammatory; antiulcer; vulnerary; anticonvulsant; antibacterial; antifungal; antiparasitic; cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder; neurological disease; infection; human; secreted protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      02-AUG-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200155367-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        musculoskeletal system; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human musculoskeletal system related polynucleotide SEQ ID NO 2897.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAL36532 standard; DNA; 7601 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the cDNA. The full length clones were obtained by construction of full length enriched cDNA libraries that were synthesised by the oligo-capping method. The primers enable the production of the full length cDNA easily without any special methods. The present sequence is a full length human cDNA of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in CD-ROM format directly from EPO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1838 BP; 404 A; 565 C; 468 G; 401 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15.8%;
1 Similarity 67.1%;
47; Conservation
                    2000US-0220964
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2000US-0216487
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2000US-0189874
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Pred. No. 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   _DB 22; Length 1838;
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        14 SEP - 2000
21 SEP - 2000
25 SEP - 2000
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27 SEP - 2000
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27 SEP - 2000
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28 SEP - 2000
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14-AUG-2000)
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14-AUG-2000)
18-AUG-2000)
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22-AUG-2000)
22-AUG-2000)
23-AUG-2000)
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01-SEP-2000]
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2000US-0237040
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2000US-0234998
2000US-0235484
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2000US-0225447.
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2000US-0225759.
2000US-0225759.
2000US-0225759.
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08-NOV-2000;
08-NOV-2000;
08-NOV-2000;
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17-NOV-2000;
17-NOV-2000;
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17-NOV-2000;
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2000US-0246613.
2000US-0249207.
2000US-0249208.
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2000US-0246532.
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2000US-0250391.
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2000US-0249297.
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2001US-0259678.
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2000US-0251868.
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                                                                                                                                                                                                          2000US-0251990
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(HUMA-) HUMAN GENOME SCI INC

Barash SC,

2001-451937/48.

Isolated polypeptide for treating, preventing and/or prognosing disorders related to the musculoskeletal system including musculoskeletal cancers and also for testing and detection e.g. diagnosis

Example 2; SEQ ID NO 2897; 781pp + Sequence Listing; English

CC (ABB03087-ABB04109) associated with the musculoskeletal system useful CC (ABB03087-ABB04109) associated with the musculoskeletal system useful CC for preventing, treating or ameliorating medical conditions e.g. by GC for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human CC tissues disclosed in the specification. The nucleic acids, proteins, CC antibodies and (ant)agonists are useful in the diagnosis, treatment CC antibodies and (ant)agonists are useful in the diagnosis, treatment CC discrears of the adrenal gland, bone, bone marrow, breast, CC discrears e.g. Addison's disease, allergies, autoimmune haemolytic consenta, autoimmune thyroiditis, diabetes multitus, Crohn's disease, CC anaemia, autoimmune thyroiditis, diabetes multitus, Crohn's disease, CC cardiovascular disorders such as myocardial ischaemias; (d) wound the control of the co parasitic infections.

Note: The sequence data for this patent did not form part of the parinted specification, but was obtained in electronic format directions specification, but was obtained in the sequences.

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Sequence 7601 BP; 2275 A; 1450 C; 1551 G; 2325 T; 0 other;
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printed specification, but was obtained in electronic from WIPO at ftp.wipo.int/pub/published\_pct\_sequences.

format directly

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RESULT 11
AAL36533
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6540 AACACT 6545
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24-FEB-2000;
02-MAR-2000;
16-MAR-2000;
17-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                         Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral; antiallergic; hepatotropic; antidiabetic; antiinflammatory; antiulcer; vulnerary; anticonvulsant; antibacterial; antifungal; antiparasitic; cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder; neurological disease; infection; human; secreted protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human musculoskeletal system related polynucleotide SEQ ID NO 2898
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 08-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAL36533 standard; DNA;
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                                                                                                                   26-JUL-2000;
26-JUL-2000;
14-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                   musculoskeletal system; ds
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                                                                                                                                                                                                                                 19-MAY-2000;
07-JUN-2000;
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                                                                                                                                                                                                                                                                                                                                                                                       WO200155367-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                       31-JAN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    69
                                                                                                                                                                                                                                                      18-APR-2000;
                                                                                      14-AUG-2000;
14-AUG-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GAGGAAATTATGGGTGTAATTGGAGTCACTGAAGGAGGAGTGGAGGCAGGAGCAGAAAA 6539
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                        2000US-0198123.
2000US-0205515.
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2000US-0225270
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 Mismatches

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Pred. No. 2.3;
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14-SEP-2000;
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08-SEP-2000;
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08-DEC-2000
08-DEC-2000
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                                                                                                                                                                                                                                      (HUMA-) HUMAN GENOME SCI INC
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17-NOV-2000;
17-NOV-2000;
17-NOV-2000;
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2000US-0249211.
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2000US-0249207
                                                                                                                                                                                                                       Ruben SM;
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Isolated polypeptide for treating, preventing and/or prognosing disorders related to the musculoskeletal system including musculoskeletal cancers and also for testing and detection e.g.

Example 2; SEQ ID NO 2898; 781pp + Sequence Listing; English.

for preventing, treating or ameliorating medical conditions e.g. by
C protein or gene therapy. The genes are isolated from a range of human
C antibodies and (antiagonists are useful in the diagnosis, proteins,
C and prevention of: (a) cancer, e.g. breast and ovarian cancer and
C gastrointestinal tract, liver lung, or urogenital; (b) immune
C anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease,
C multiple sclerosis, rheumatoid arthritis and ulcerative colitis;
C c) cardiovascular disorders such as myocardial isohaemias; (d) wound
C and (f) infectious diseases such as myocardial anoxia and epilepsy;
C naraesitic infections diseases such as viral, bacterial, fungal and parasitic infections. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directions. The invention relates to novel genes (AAL34669-AAL37666) and proteins (ABB03087-ABB04109) associated with the musculoskeletal system useful pecification, but was obtained in electronic format directly
at ftp.wipo.int/pub/published\_pct\_sequences.

Sequence 7601 BP; 2275 A; 1450 C; 1551 G; 2325 T; 0 other;

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Query Match
Best Local
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             y Match 15.8%;
Local_Similarity 54.0%;
     68; Conservative
Score 33.2; DB Pred. No. 2.3; 0; Mismatches
                    DB 22; Length 7601;
 58;
 Indels
 0;
Gaps
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RESULT 12
AAL03820/c
ID AAL038
XX
AAL03820/c
ID AAL038
XX
AC AAL038
AC AAL03
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RESULT 13
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Best Local Similarity
Matches 47; Conserv
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4760 GCCGGGAAGG 4751
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                                                                                                                                       AAL04727;
                                                                                                                                                                                                                                                            Sequence 11360 BP; 2899 A; 2709 C; 2708 G; 3044 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                            The present invention provides the protein and coding sequences of a number of human reproductive system related antigens. These can be used in the prevention and treatment of reproductive system disorders, including cancer. The present sequence is a genomic sequence encoding a protein of the invention.
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17-NOV-2000;
17-NOV-2000;
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17-NOV-2000;
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17-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; SEQ ID NO 6508; 1297pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Isolated nucleic acid molecule encoding a reproductive system antigen is used in preventing, treating or ameliorating a medical condition
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                                                                                                                                                                                                                                                                                  reproductive system related antigen; reproductive system disorder; gene therapy; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention provides the protein and coding sequences of a number of human reproductive system related antigens. These can be used in the prevention and treatment of reproductive system disorders, including cancer. The present sequence is a genomic sequence encoding a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Isolated nucleic acid molecule encoding a reproductive system antigen is used in preventing, treating or ameliorating a medical condition
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Odorant receptor; fruit fly; DOR62; odour recognition; pest control;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Drosophila melanogaster odorant receptor DOR62 coding sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAA94801;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAA94801 standard; DNA;
The present sequence is the coding sequence for the Drosophila melanogaster odorant receptor DOR62. It was isolated using a differential cloning strategy. The odorant genes and proteins are useful as they ald in the study of the olfactory organ in mammals, as well as aiding the understanding of the link between odour recognition and behaviour in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23-FEB-2001
                                                                                                               Novel nucleic acid encoding an insect odorant receptor, for identifying modulator compounds that are useful in controlling pest population
                                                                                                                                                                                                                                                                                     25-FEB-2000; 2000WO-US04995
                                                                                                                                                                                                                                                                                                                                            WO200050566-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Drosophila melanogaster.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 119 GCCGAGAAGG 128
                                                                                    Claim 4; Fig 8; 176pp; English.
                                                                                                                                                           P-PSDB;
                                                                                                                                                                         WPI; 2000-572081/53.
                                                                                                                                                                                                   Vosshall LB,
                                                                                                                                                                                                                                                          25-FEB-1999;
                                                                                                                                                                                                                              (UYCO ) UNIV COLUMBIA NEW YORK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       59
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                                                                                                                                                          AAB26401
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                                                                                                                                                                                                   Amrein HO,
                                                                                                                                                                                                                                                          9908-0257706
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                                                                                                                                                                                                                                                                                                                                                                                        "DOR62"
                                                                                                                                                                                                      Axel R;
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01-DEC-01-DEC-05-DEC-05-DEC-

Rosen CA,

Barash SC,

Ruben SM;

17-NOV-

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RESULT 15
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The invention relates to primers for synthesising full length cDNA clones. 830 cDNA molecules encoding a human protein have been isolated and nucleotide sequences of 5'- and 3'-ends of the cDNA molecules have been determined. Primers for synthesising the full length cDNA are useful for clarifying the function of the protein encoded by the cDNA. The full length clones were obtained by construction of full length enriched cDNA libraries that were synthesised by the oligo-capping method. The primers enable the production of the full length cDNA easily
                                                                                                                            Claim 3; SEQ ID NO 1233; 1380pp + sequence listing; English
                                                                                                                                                                      830 Primers useful for synthesizing full length cDNA clones
                                                                                                                                                                use in genetic manipulation
                                                                                                                                                                                                          WPI; 2001-524255/58.
                                                                                                                                                                                                                                       Wakamatsu A,
                                                                                                                                                                                                                                                       Ota T,
                                                                                                                                                                                                                                                                               (HELI-) HELIX RES INST.
                                                                                                                                                                                                                                                                                                                        08-JUL-1999;
11-JAN-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; full length cDNA; cDNA synthesis; oligo-capping; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human cDNA 3'-end sequence, SEQ ID NO: 1233.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     06-NOV-2001 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     insects. They also enable the identification of compounds capable of activating and inhibiting the receptors, allow the control of pest populations via the use of alarm odour ligands and via the use of ligands which interfere with the interaction between odorant ligands and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               receptors associated with fertility.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                122 GAGAAGGAACTCTGAAGACTCCGTAGATTGCTCTAGACCGCCTCAGACACTCTCGGCGCA 181
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2000JP-0118774.
2000JP-0183765.
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T, Koga H;
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                                                                                                                                                                                                                                                                                                                                                                                                              without any special methods. The present sequence is the nucleotide sequence of the 3'-end of a cDNA provided in the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in CD-ROM format directly from EPO.
                                                                                                                                                                                                                                                                                                                                                                             Sequence 555 BP; 124 A; 148 C; 167 G; 110 T; 6 other;
                                                                     205 GCCCTTAGTGAGGTGTCACCTCTCCCAGAGTCACAGGACGCTTCTGGGA
                                                                                                                                            145 CCCCAGATGTAGGGGAGGCCTGATTCGCATCGGGGCCGGGCGCGTTACTCCATGGGGTCG
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                                                                                                                                                                                TCCCTGCTTTTGGGGGGGGAGGGGGGGGGGATGAGCCAGGGCCGAGAAGGAACTCTGAAG 138
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Copyright (c) 1993 - 2002
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Compugen Ltd.
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AA42260 vd29d10.s
AZ406458 1M0175007
BIB44815 fq14c10.x
AL51339 AL515339
AL249035 Tetraodon
AZ40888 1M0180922
AL331393 Tetraodon
BH106958 RPCI-24-2
BH113183 RPCI-24-2
BH113183 RPCI-24-2
                                                                                                                                    AZ971837 2M0245B02
AL258341 Tetraodon
AL196781 Tetraodon
AZ463187 1M0271B21
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AZ394294 1M0157J18
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HAZASOO BHZOSOF CNSOJFZH AZ967532 AZ32426 CNSOSDQZ AAO78583	AZ340230 BH315615 CNS053B9 CNS0241WD CNS02H50 AZ101812 CNS0300G CNS0300G CNS04G1P CNS04G1P	AZ902149 BM156047 FR0008122 CNS03XZZ CNS051R1 CNS0574 AZ377122 AZ777122 AZ783123 BH097540 W54246 BG009448
BH3203013 CH320-159 BH320813 CH320-159 AL242342 Tetraodon A2967352 2M0238F05 AZ3372426 IM0060172 AL332756 Tetraodon AA078583 7P05H08 C		AZ902149 RPCI-24-1 BM156047 fv18a04.x Z91932 F.rubripes AL165688 Tetraodon AL339238 Tetraodon AL213279 Tetraodon AZ22674 RPCI-23-4 AZ377122 1M0131L14 AZ783123 2M0024K04 BH097540 RPCI-24-2 W54246 Gmc944h1.r1 BG069448 H3075F07-

## ALIGNMENTS

ACCESSION VERSION KEYWORDS SOURCE REFERENCE AUTHORS LOCUS DEFINITION RESULT 1 AZ971837/c COMMENT FEATURES TITLE ORGANISM JOURNAL source Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.0
Plate: 0245 row: B column: 02
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends 689 bp DNA linear GSS 27-APR-2012M0245B02R Mouse 10kb plasmid UUGC2M library Mus musculus genomic clone UUGC2M0245B02 R, DNA sequence. 1 (bases 1 to 689)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Rei University of Utah Genome Center University of Utah Rm. 308, Biomedical Polymers Res Unpublished (2000) Contact: Robert B. ,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R. Mus musculus AZ971837 High quality sequence stop: 689 84112, plasmid inserts Mouse whole genome scaffolding with paired end reads from 10kb Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus AZ971837.1 touse mouse USA /organism="Mus musculus"
/strain="C57BL/6J"
/db\_xref="ftaxon:10090"
/clone="UUGC2M0245B02"
/clone\_lib="Mouse 10kb plasmid UUGC2M library" Location/Qualifiers GI:13843064 . 689 Weiss Polymers Research Bldg., Std Error: 0.00 20 Pedersen, T., Reilly ŝ 2030 GSS 27-APR-2001 EI . SLC, Ţ

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Query Match
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TGAGAAACTTG 1594
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    669;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
189 c 147 g 180 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             adaptored DNA was purified and size-selected for a 9.5 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (female) was obtained from the Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Laboratory Mouse DNA Resource
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /sex="Female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           40.28;
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Pred. No. 4.2e-134;
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                                                                           CNS02GTW/c
                      DEFINITION
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                                                     LOCUS
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509

1044

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ORIGIN BASE COUNT

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689

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Tetraodon nigroviridis genome survey sequence PUC-Ori end of clone 138G22 of library G from Tetraodon nigroviridis, genomic survey

681 bp

DNA

linear

GSS 13-MAY-2000

CNS02GTW

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                                     ACACATGTTTTCTTCCCTCC 294
                                                                             GCTGCTCTGTCCACCGCCAGCCTGGCTTCAATCAGCCCCAGGAACGTGTGAGGRGGKCCA 766
                                                                                                                                                                                                  GGTGCTTTCTCCCCCACCATGCGACCCGGGAGCTCCACTGATATGGACAGAATAGCTTTA 214
  ACTCATGAGGTCATCCCTCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (12-APR-2000) to the EMBL/GenBank/DDBJ databases This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Roest-Crollius, H., Jaillon, O., Dasilva, C., Bouneau, L., Fisher, C., Bernot, A., Fizames, C., Wincker, P., Brottier, P., Quetier, F., Saurin, W. and Weissenbach, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bouneau,L., Billault,A., Quetier,F., Saurin,W., Bernot,A. Weissenbach,J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
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Tetraodon nigroviridis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          946 bp DNA linear GSS 17-MAY-2000 Tetraodon nigroviridis genome survey sequence T7 end of clone 051520 of library G from Tetraodon nigroviridis, genomic survey sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Genoscope
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished
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st-Crollius, H., Jaillon, O., Dasilva, C., Fizames, C., Fisher, C.,
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                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                      /organism="Tetraodon nigroviridis"
/db_xref="taxon:99883"
/clone="051620"
/clone_1ib="G"
/note="Genoscope sequence ID : C0BG051BD10LP1-end : T7"
/ 291 c 305 g 133 t 26 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                        CCCTCCCTCCACTTCCTCCCATTCTCTGTGGTCC 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                               sequence.
AL196781
AL196781.1 GI:7834931
AL196781.1 GI:7834931
GSS; genome survey sequence.
Tetraodon nigroviridis.
Tetraodon nigroviridis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Actinopterygii, Neopterygii; Percomorpha; Tetraodontiformes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (12-APR-2000) to the EMBL/GenBank/DDBJ databases This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetracdon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetracdon.
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Bouneau,L., Billault,A., Quetier,F., Saurin,W., Bernot,A. and
Weissenbach,J.
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
                                                                          Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia; 1 (bases 1 to 511)
                                                                                                                                                                               Az463187.1 GI:10621312 GSS.
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                                                                                                                                                                                                                                        1M0271B21R Mouse 10kb plasmid ÜUGC1M library Mus musculus genomic
clone UUGC1M0271B21 R, DNA sequence.
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                                                                                                                                        Mus musculus
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                                                                                                                                                              house mouse.
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/note="Genoscope sequence ID :
pUC-Ori"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Tetraodon nigroviridis"
/db_xref="taxon:99883"
/clone="138G22"
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81.9%;
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Pred. No. 0.00033;
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                                                                                                                                                                                                                                                                                511 bp
                                                                                                Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            166 t
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Qγ 밁

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KEYWORDS VERSION

ACCESSION

sequence. AL233144

AL233144.1

genome survey sequence

GI:7892279

DEFINITION

Tetraodon 006A06 of

nigroviridis genome

958 bp

DNA

library G from Tetraodon nigroviridis, genomic survey

survey sequence

linear G

GSS 15-MAY-2000 d of clone

CNS038VZ

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JOURNAL COMMENT
CNS038VZ/c
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                                                                                                                                                                                                                                                                      Local
                                                                                                                                  TTCCTCCCATTCTCT 315
                                                                                                                                                                                                                        Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunnegenetics.utah.edu
                                                                                                                                                                                                                                                                                                                                                             l Similarity 68.1
92; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Insert Length: 10000 Std Error: Plate: 0271 row: B column: 21 Seq primer: CACACAGGAAACAGCTATGACC
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University of Utah
Rm. 308, Biomedical Polymers Research Bldg.,
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Contact: Robert B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 High quality sequence stop: 511.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Class: plasmid ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  plasmid inserts
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gil4732114|gb\AF129072.1), a copy-number inducible derivative of plasmid Rl. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     was hydrodynamically sheared by repeated passage through 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone_lib="Mouse 10kb plasmid UUGC1M library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /strain="C57BL/6J"
/db_xref="taxon:10090"
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                          ACACACACACACACACACACACACACACGCTTT 547
                                                                                                                                                                                                                                                                                                                                                                                        ACACACACACACACACACACACACATGTTTT 285
                                                                                                                                                                                                                                                                                                                                                                                                                          ATGAAAGAAATCTACGATGACAGTTTGATACCTTGTCCAGAAGGGGGCAGCACCGGCAC 642
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (12-APR-2000) to the EMBL/GenBank/DDBJ databases This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 (bases 1 to 958)
Roest-Crollius, H., Jaillon, O., Dasilva, C., Bouneau, L., Fisher, C., Bernot, A., Fizames, C., Wincker, P., Brottier, P., Quetier, F., Saurin, W. and Weissenbach, J.
Human gene number estimate provided by genome wide analysis using Tetracdon nigroviridis DNA sequence
                   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 684)
                                                                                                                                           Mus musculus
                                                                                                                                                                                                                AZ394294 684 bp DNA linear GSS 03 IM0157J18R Mouse 10kb plasmid UUGC1M library Mus musculus clone UUGC1M0157J18 R, DNA sequence.
AZ394294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bouneau,L., Billault,A., Quetier,F., Saurin,W., Bernot, Weissenbach,J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes; Tetraodontidae; Tetraodon.
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Roest-Crollius, H., Jaillon, O.,
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whole genome scaffolding with paired end reads from 10kb
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/clone_lib="G"
/note="Genoscope sequence
/note="Genoscope sequence
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/clone="006A06"
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                                                                                                                                                                                                  GI:10509366
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Pred. No. 0.00066;
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4 others
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155 GGTGCTTTCTCCCCCACCATGCGACCCGGGAGCTCCACTGATATGGACAGAATAGCTTTA 214
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GSS; genome survey sequence. Tetraodon nigroviridis.
                                                     AL175958.1 GI:7814015
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Location/Qualifiers
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Insert Length: 10000 Std Erro
Plate: 0157 row: J column: 1:
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Fax: 801 585 7177
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University of Utah
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Unpublished (2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The
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/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
                                                                                                                                 nigroviridis genome surve
library G from Tetraodon
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/clone="UUGC1M0157J18"
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Pred. No. 0.00073;
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Roest-Crollius, H., Jaillon, O., Dasilva, C., Fizames, C., Fisher, C. Bouneau, L., Billault, A., Quetier, F., Saurin, W., Bernot, A. and Weissenbach, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (12-APR-2000) to the EMBL/GenBank/DDBJ databases This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.
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Bernot, A., Fizames, C., Wincker, P., Brottier, P., Quetier, F.,
Saurin, W. and Weissenbach, J.
                                                                                                                                                 1 (bases 1 to 398)
Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubu, Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,
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AA422680.1 GI:2101558
EST.
                                                                                                                                                                                                                                                                                                                                                                                                AA422680 398 bp vd29d10.sl Knowles Solter mouse 2 IMAGE: 793939 5', mRNA sequence.
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                                       Unpublished (1996)
Contact: Marra M/Mouse EST Project
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Washington University School of MedicineP
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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/clone_lib="G"
/note="Genoscope sequence ID : C0AG224AD08LP1-end : T7"
/note="Genoscope sequence ID : C0AG224AD08LP1-end : T7"
/ 217 c 184 g 132 t 46 others
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/db_xref="taxon:99883"
/clone="224G15"
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                                                                                        Contact: Robert B. University of Utah University of Utah
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4444 Forest Park Parkway, Box 8501,
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                           Mus musculus
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                   Tel: 801 585 5606 Fax: 801 585 7177
                                                                                                                                                   Unpublished (2000)
                                                                                                                                                                                     Mouse whole genome scaffolding with paired end reads
                                                                                                                                                                                                         and Wright, D., Weiss, R
                                                                                                                                                                                                                      Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Email: ddunn@genetics.utah.edu
                                                                                                                                                                                                                                                                                                                                                           house mouse
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                                                                                                                                                                   inserts
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                                                                          Biomedical Polymers Research Bldg.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone_lib="Knowles Solter mouse 2 cell"
/tissue_type="embryo"
/dev_stage="2-cell"
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/db_xref="taxon:10090"
/clone="IMAGE:793939"
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70.2%;
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Pred. No. 0.0009;
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Std Error: 0.00

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Clark,M., Johnson,S.L., Lehrach,H., Lee,R., L1,F., Marra,M., Eddy,S., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter,E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                      BI844815
547 bp mRNA linear EST 04-OCT-2001 fq14c10.x1 zebrafish adult brain Danio rerio cDNA clone 4831482 3/ similar to TR:09UMF8 Q9UMF8 TRANSALDOLASE ;contains element MER35 repetitive element ;, mRNA sequence.
BI844815
  Unpublished (1998)
Contact: Stephen L
                                                  WashU Zebrafish EST Project 1998
                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Seq primer: CACACAGGAAACAGCTATGACC Class: plasmid ends High quality sequence stop: 556.
                                                                            and Wilson, R.
                                                                                            Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pNA02 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
Stephen L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (http://www.jax.org/resources/documents/dnares/). The DNA
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/clone="UUGC1M0175007"
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/strain="C57BL/6J"
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Contact: Genoscope
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Full-length cDNA libraries and
                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 589)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cDNA Library Preparation: John Ngai. cDNA Library Arrayed by: Matthew Clark. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: Genome Systems, St. Louis, Missouri (web address: www.genomesystems.com) (email contact: info@genomesystems.com) and Research Genetics, Huntsville, Alabama (web address: www.resgen.com) (email contact: info@resgen.com) and RessourcenZentrumPrimarDatenbank, Berlin, Germany (web address:
                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
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Fax: 314 286 1810
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4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         mRNA sequence.
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/note="Vector: pZIPLOX; Site_1: Not1; Site_2: Sall;
Original library was constructed in lambdaZIPLOX. Nexcision of the cDNA library was performed to yield pZIPLOX plasmids. Insert check was done in original library."

152 c 98 g 107 t 1 others
                                                             /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="LTI_NFL006_PL2"
/tissue_type="placenta"
                                            /clone="CL0BB029ZG08"
                                                                                                                             Location/Qualifiers
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/sex="mixed male and female"
/tissue_type="brain"
/dev_stage="adult"
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/db_xref="taxon:7955"
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Pred. No. 0.0011;
0; Mismatches 16;
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                                                                                                                                                                                                                                                                                                                                                                        Roest-Crollius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C., Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F., Saurin,W. and Weissenbach,J.
Human gene number estimate provided by genome wide analysis using Textaodon nigroviridis DNA sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bouneau,L., Billault,A., Quetier,F., Saurin,W.,
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                                          /organism="Tetraodon nigroviridis'
/db_xref="taxon:99883"
                       /clone="034P14"
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/clone_lib="G"
                                                                                                                           Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Erro
Plate: 0180 row: P column: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Robert B. Weiss
University of Utah Genome
University of Utah
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tel: 801 585 5606
Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mouse whole genome scaffolding with paired end reads from 10kb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
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Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae;
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                                                                                                                                                                                                                                                                                                                                                                                                     Class: plasmid ends
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              (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velty. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected
                                                                                                                                          Laboratory Mouse DNA Resource
                                                                                                                                                          /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson
                                                                                                                                                                                                                                   /db_xref="taxon:10090"
/clone="UUGC1M0180P22"
/clone_1ib="Mouse 10kb plasmid UUGC1M library"
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1 274 c 246 g 221 t 3 others
                                                                                                                                                                                                                                                                                                  /organism="Mus musculus"
/strain="C57BL/6J"
                                                                                                                                                                                                                     /sex="Male"
                                                                                                                                                                                                  /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
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                                                                                                                                                                                Submitted (12-APR-2000) to the EMBL/GenBank/DDBJ databases This sequence is a single read and was generated as part of a law scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at
                                                                                                                                                                                                                                                                                                                                                              Human gene number estimate provided by genome Tetraodon nigroviridis DNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                           2 (bases 1 to 957)
Roest-Crollius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C.,
Bernot,A., Fizames,C., Wincker,P., Brottler,P., Quetler,F.,
Saurin,W. and Weissenbach,J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished
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                                                                                                                                                           http://www.genoscope.cns.fr/Tetraodon.
                                                                                                                                                                                                                                                                              Direct Submission
                                                                                                                                                                                                                                                                                                   Genoscope.
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a 162 c 122 g 202 t
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                                            /organism="Tetraodon nigroviridis'
/db_xref="taxon:99883"
/clone="020P23"
/note="Genoscope sequence ID : C0AA020CH12A2~end : T3"
                         /clone_lib="A"
                                                                                                                                        Location/Qualifiers
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Pred. No. 0.0012;
""smatches 53;
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Quetier,F., Saurin,W.,
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Contact: Shaying Thao
Contact: Shaying Thao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, M
Tel: 301 838 0200
Fax: 301 838 0208
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  (pdejong@mail.cho.org). Clones may be purchased from BACPAC Resources (http://www.chori.org/bacpac/orderingframe.htm). BAC page: http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html Plate: 264 row: G column: 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: szhao@tigr.org
Email: szhao@tigr.org
Clones are derived from the mouse BAC library RPCI-24. For BAC
Clones are derived from the mouse BAC library RPCI-24. For BAC
Library availability, please contact Pieter de Jong
(pdejong@mail.cho.org). Clones may be purchased from BACPAC
(pdejong@mail.cho.org). Clones may be purchased from BACPAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Zhao,S., Nierman,W., Malek,J., Shatsman,S., A)
Tsegaye,G., Geer,K., Krol,M., Shvartsbeyn,A.,
Russell,D., de Jong,P. and Fraser,C.M.
Mouse BAC End Sequences from Library RPCI-24
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Class: BAC ends.
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                                                                                                                                                                          DNA.
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/clone="RPCI-24-264G24"
/clone_lib="RPCI-24"
                                                                                                                                                                                                                                                                                                                                                  /organism="Mus musculus"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                             /cell_type="Spleen/Brain"
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Sequence 7 from Patent W00179290.
AX354813
AX354813.1 GI:18619545
                                                                                    Glp-2 receptor gene promoter and uses thereof Patent: WO 0179290-A 7 25-OCT-2001; 1149336 ONTARIO INC. (CA)
                                                                                                                                                               Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                   Drucker, D.J. and Lovshin, J.A.
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              /organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         181 AGCGTGGAGAGGATTTGTGCAAACATTTCC 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 CGAGAAGGAACTCTGAAGACTCCGTAGATTGCTCTAGACCGCCTCAGACACTCTCGGCGC 180
                                                                                                                                                                                                                                                                                                                                                  Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Anderson, S., Baldwin, J., Barna, N., Bastien, V., Beda, F., Boguslavkiy, L., Boukhgalter, B., Brown, A., Burkett, G., Campopiano, A., Castie, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Domino, M., Doyle, M., Ferreira, P., Fitzhugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L., Gardyna, S., Ginde, S., Goyette, M., Graham, L., Grand-Pherre, N., Grant, G., Hagos, B., Heaford, A., Horton, L., Klein, J., LaRocque, K., Lamazares, R., Landers, T., Leboczky, J., Levine, R., Lieu, C., Liu, G., Locke, K., Macdonald, P., Marquis, N., McCarthy, M., McEwan, P., McGurk, A., McKernan, K., McPheeters, R., McCarthy, M., McEwan, P., McGurk, A., McRernan, K., McPheeters, R., Meddrim, J., Maneus, L., Mihova, T., Miranda, C., Menga, V., Morrow, J., Peterson, K., Pierre, N., Plsani, C., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Tirrell, A., Travers, M., Trigilio, J., Yeong, G., Zainoun, J., Zimmer, A., and Zody, M.
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------ Genome Center
                                                                                                                                                                                                                   Submitted (22-MAR-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Aug 26, 2001 this sequence version replaced gi:14547870. All repeats were identified using RepeatMasker:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutherla; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 198271)
Birren,B., Linton,L., Nusbaum,C. and Lander,E.
                                                                                                                                                                                                           Smit, A.F.A. & Green, P. (1996-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens chromosome 17, clone RP11-655D3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HTG; HTGS_PHASE2; HTGS_FULLTOP; HTGS_ACTIVEFIN
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                (bases 1 to 198271)
Center project name: L8450
                                                                                                                               Center: Whitehead Institute/ MIT Center for Genome Research
                                                                                                         Center code: WIBR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4 ordered pieces.
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SEQUENCING
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REFERENCE
AUTHORS
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AC087646/c
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KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Db 144273 CCGCCTTGTTCTTCTCCTCAGCCTGTCAAGGAAGTCCCAGAAAGCACAGCTGACTTAGG 144214
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                                                                                                                                                                                                            AUTHORS
TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CGAGAAGGAACTCTGAAGACTCCGTAGATTGCTCTAGACCGCCTCAGACACTCTCGGCGC
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Birren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, S. Barna, N., Bastien, V., Boguslavkiy, L., Boukhgalter, B., Brown, A., Camarata, J., Campopiano, A., Choepel, Y., Coalgelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Dlaz, J.S., Dodge, S., Faro, S., Ferreira, P., Fitzhugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L., Grand-Pierre, N.,
                                                                                                                                                                                                                                                                                                                                                                                                                               210719 bp DNA linear HTG 31-MAY-200: HOMO sapiens chromosome 17 clone RP11-773021 map 17, WORKING DRAFT SEQUENCE, 12 unordered pieces.
ACO87646
                                                                                                                                                                          Homo sapiens chromosome 17, clone RP11-773021
Unpublished
                                                                                                                                                                                                                            Birren, B., Linton, L., Nusbaum, C. and Lander, E.
                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                               AC087646.3 GI:14269760
                                                                                                                                                                                                                                                                                                                                                                human.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This sequence will be replaced
by the finished sequence as soon as it is available and
the accession number will be preserved.
1 153566: contig of 153566 bp in length
153567 153666: gap of 100 bp
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                                                                                                                                                     (bases 1 to 210719)
                                                                                                                                                                                                                                                       (bases 1 to 210719)
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158889 158988: gap of
158989 189474: contig of 30486 bp in length
189475 189574: gap of
189575 198271: contig of 8697 bp in length.
                                                                                                                                                                                                                                                                                                                                                                                  HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Center clone name: 655_D_3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone_lib="RPCI-11 Human Male BAC"
45543 c 46237 g 53270 t 363 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /db_xref="taxon:9606"
/chromosome="17"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone="RP11-655D3"
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                                                                                                                                                                                                                                                                                 Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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                                                                                                                           Anderson, S.,
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Lehoczky, J., Levine, R., Liu, G., MacLean, C., Macdonald, P., Marquis, N., Matthews, C., McCarthy, M., McEwan, P., McKernan, K., McCheeters, R., Meldrim, J., Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Retta, R., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Resta, R., Rieback, M., Riley, R., Rise, C., Rogov, P., Roman, J., Rosetti, M., Raley, R., Schauer, S., Schupback, R., Seaman, S., Severy, P., Sougnez, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Travers, M., Travis, N., Trigillo, J., Vassiltev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W. J., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Research, 320 Charles Street, Cambridge, MA 02141, USA ON May 31, 2001 this sequence version replaced gi:13493095. All repeats were identified use peatmasker: Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hagos, B., Heaford, A., Jones, C., Karatas, A.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               * NOTE: This is a 'working draft' sequence. It currently * consists of 12 contigs. The true order of the pieces * is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence
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                                                                                                                                                                                                                                                                                                              75254 contig of 75254 bp in length
75255 75354; gap of
75355 76881; contig of 1527 bp in length
76882 76981; gap of
76882 76981; gap of
76882 76981; gap of
76882 76981; gap of
78538 contig of 1557 bp in length
78539 78538; gap of
78539 79946; contig of 1308 bp in length
78539 79946; contig of 1308 bp in length
79947 80046; gap of
82098 contig of 2052 bp in length
82099 82198; gap of
82099 82198; gap of
82199 86309; contig of 4111 bp in length
86410 89601; contig of 3192 bp in length
86410 89601; contig of 3192 bp in length
88602 89701; gap of
89602 89701; gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequencing vector: Plasmid; n/a; 100% of reads Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.960731
Consensus quality: 205962 bases at least Q40
Consensus quality: 208431 bases at least Q30
Consensus quality: 208109 bases at least Q30
                                        121202
154072
154172
193986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Quality coverage: 8.4 in Q20 bases; agarose-fp Quality coverage: 8.2 in Q20 bases; sum-of-contigs
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Center clone name: 773_0_21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Center code: WIBR
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Insert size: 209619; sum-of-contigs
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154171: gap of 100 bp
19398: contig of 39814 bp in length
194085: gap of 100 bp
210719: contig of 16634 bp in length
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                                                                                                                                  ACU69006 213359 bp DNA linear HTG 11-DEC-20 Homo sapiens chromosome RPCI-11 clone RP11-773021, WORKING DRAFT SEQUENCE, 16 unordered pieces.
1 (bases 1 to 213359)
                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                   Homo sapiens
                                                                                                        AC069006.4 GI:11612641
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154172. .193985
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194086. .210719
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/note="assembly_fragment"
80047. .82098
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89702. .105000
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121202. .154071
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105101. .121101
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/db_xref="taxon:9606"
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                source
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Insert size: 211859; sum-of-contigs
Quality coverage: 5.34 in Q20 bases; agarose-fp
Quality coverage: 5.44 in Q20 bases; sum-of-contigs
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Submitted (16-MAY-2000) Genome
University School of Medicine,
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The sequence of Homo sapiens clone
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         as soon as it is available and the accession number will be preserved.
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) Dec 11, 200
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∕organism="Homo sapiens"
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117462: contig
117562: gap of
143519: contig
143619: gap of
                                           143619: gap of unknown length
171176: contig of 27557 bp in
171276: gap of unknown length
213359: contig of 42083 bp in
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Sequence 1 from Patent WO0179290.
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/notce="assembly_name:Contig33"
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94748. .117462
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78637. .94647
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/chromosome="RPCI-11"
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/note="assembly_name:Contig20"
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                                                                                                                                                                                                                                                                                                                  Direct Submission
Submitted (17-JAN-2001) Department of Medicine, University of
Toronto, 101 College Street CCRW3-845, Toronto, ON M5G2C4, Canada
                                                                                                                                                                                                                                                                                                                                                                                                                                          Glucagon-like Peptide (GLP)-2 Action in the Murine Central Nervous System Is Enhanced by Elimination of GLP-1 Receptor Signaling J. Biol. Chem. 276 (24), 21489-21499 (2001)
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/db_xref="taxon:32630"
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                                  /product="glucagon-like peptide-2 receptor"
/protein_id="AAK63043.1"
/db_xref="GI:14485647"
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/strain="129/SvJ"
/db_xref="taxon:10090"
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                    translation="MRRLWGPGTPFLSLLLLVSIKQ"/
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                                                                                                                                                                                                                                                                                                                                                                             Submitted (30-NOV-1999) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA on Mar 1, 2000 this sequence version replaced gi:6970326.
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Birren,B., Linton,L., Nusbaum,C. and Lander,E.
Mus musculus chromosome 11, clone RP23-409J21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                                                                      http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished
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                     Conservative
                                                                                                                                                                                                                            Center code: WIBR
                                                                                                                                                                                                                                                      Center: Whitehead Institute/ MIT Center for Genome Research
                                                                                                                                                                                                     Web site: http://www-seq.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HTGS_PHASE1; HTGS_DRAFT
Assembly program: Phrap; version 0.960731
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                                                                                                                                                                                                                                                                                   -- Genome Center
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Pred. No. 1.9e-08;
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                               100% of reads
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Consensus quality: 196848 bases at least Q40 Consensus quality: 202204 bases at least Q30 Consensus quality: 204082 bases at least Q20 Insert size: 210000; agarose-fp onality coverage: 4.8 in Q20 bases; agarose-fp onality coverage: 4.9 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        149263 149362: gap of 100 bp 1149263 177577: contig of 28215 bp in length
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40234 482
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31996 32095:
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10638 14144: contig of 3507 b
14145 14244: gap of 100 bp
14245 18479: contig of 4235 b
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642 1859: contig of 1218 bp in length
1860 1959: gap of 100 bp
1960 4152: contig of 2193 bp in length
4153 4252: gap of 100 bp
6291: contig of 2039 bp in length
                                              1960.
                                                                                                                                                                                         clone_end:T7
/note="assembly_fragment"
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/clone_lib="RPCI-23 Female Mouse BAC"
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/db_xref="taxon:10090"
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25538: contig of 6959 bp
5638: gap of 100 bp
31995: contig of 6357 bp
2095: gap of 100 bp
40133: contig of 6038 bp
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207160: contig of 29483 bp in length
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10537: contig of 4146 bp in length
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contig of 16221 bp in length
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RESULT 8
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                    ORGANISM
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Best Local Similarity
                                                                                                                                                                                                           28834 GCCTGAAGAGGACTTGTGCAAACACTTCC 28862
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                                                                                                                                                                                                                                         GCGTGGAGAGGATTTGTGCAAACATTTCC 210
                                                                                           AL646097 211173 bp DNA 1:
Mus musculus chromosome 11 clone RP23-338M9,
PROGRESS ***, in unordered pieces.
                Mus musculus
                                             AL646097.5 GI:18135259
HTG; HTGS_PHASE1; HTGS_DRAFT
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                 AL646097
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177678. .207160
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99582. .115973
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149363. .177577
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25639. .31995
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6392. .10537
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67.5%;
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                                                                                                            HTG 10-JAN-2002
QUENCING IN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Assembly program: XGAP4; version 4.5
sequencing vector: plasmid; L08752; 100% of reads
chemistry: Dye-terminator Big Dye; 100% of reads
consensus quality: 206626 bases at least Q40
Consensus quality: 207698 bases at least Q30
consensus quality: 208567 bases at least Q20
Insert size: 209573; sum-of-contigs
Insert size: 207120; 2.8% error; agarose-fp
Quality coverage: 9.05x in Q20 bases; sum-of-contigs Quality
coverage: 9.26x in Q20 bases; agarose-fp
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----- Summary Statistics
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: humquery@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Web site:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Center code: SC
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/note="assembly_fragment:00263
fragment_chain:1"
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/chromosome="11"
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fragment_chain:1"
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fragment_chain:1"
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                                                                                                                                                                                                                                                                                                                   /note="assembly_fragment:00672
fragment_chain:2"
                                                                                                                                                                                                                                                                                                                                                                                    /note="assembly_fragment:02994
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                                      /note="assembly_fragment:00621
fragment_chain:2"
                                                                                                          /note="assembly_fragment:01143
fragment_chain:2"
                                                                                                                                                                           /note="assembly_fragment:01861
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fragment_chain:2"
/note="assembly_fragment:00072
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Db 132359 GTCTTGCTTTTTCTTCTGGGCTTGCTGAGGAAGTCCCAGGCAGCGTAGACGTCTTGGGGG 132300
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AX354812
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AUTHORS
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ACCESSION
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                                                                  BASE COUNT
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Best Local Similarity
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                                                                                                                                                                                                                 source
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Sequence 6 from Patent W00179290.
AX354812
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                              Glp-2 receptor
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146293. .185554
/note="assembly_fragment:01439
fragment_chain:2"
nosess
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fragment_chain:2"
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                                                                                                                                                                                                                                             eceptor gene promoter and uses thereof WC 0179290-A 6 25-OCT-2001; ONTARIO INC. (CA)
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1 48310 c 47762 g
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fragment_chain:2"
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fragment_chain:2
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fragment_chain:2"
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                                                                  /translation="MRRIWGPGTPFISILLLVSIKO"
132 c 155 g 104 t 2 ot
                                                                                                 /protein_id="CAD22992.1"
/db_xref="GI:18619544"
                                                                                                                                              /note="unnamed protein product"
                                                                                                                                                                              /organism="Mus sp."
/db_xref="taxon:10095"
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Pred. No. 1.9e-08;
      Score 54; DB 6;
Pred. No. 6.3e-06;
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Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (23-AUG-2000) to the DDBJ/EMBL/GenBank databases. Takao 1809ai, Helix Research Institute, Genomics Laboratory; 1532-3 Yana, 1809ai, Chiba 292-0812, Japan (E-mail:genomics@hri.co.jp, Tel:81-438-52-3952)

MEDO human cDNA sequencing project supported by Ministry of International Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology; cDNA library construction, 5'-& 3'-end one pass sequencing and clone selection: Helix Research Institute (supported by Japan Key Technology Center (Internation of Machine).
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Homo sapiens embryo, 10 weeks whole embryo, mainly head cDNA to
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Isogai,T., Ota,T., Hayashi,K., Sugiyama,T., Otsuki,T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AK021842 mRNA linear PRI 29-SEP-2000 MRNA linear PRI 29-SEP-2000 MRNA LINEAR CONTROL OF THE PRI 2000 MRNA LINEAR C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Isogai, T. and Otsuki, T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AK021842.1 GI:10433110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (bases 1 to 1612)
                                                                                                                                                                                                                                                            352
                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   clone_lib:HEMBA1 clone:HEMBA1005931
                                                                                                                                                                                                                       /dev_stage="embryo, 10 weeks"
/tissue_type="whole embryo, mainly head"
/note="cioning vector: pME18SFL3"
476 c 391 g 393 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FINGER PROTEIN 83.
                                                                                                                                                                                                                                                                                                                                                                          /clone="HEMBA1005931"
/clone_lib="HEMBA1"
                                                                                                                                                                                                                                                                                                                                                                                                                                    /db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ocation/Qualifiers
                                                                                                      18.4%; Score 38.6; DB 9; 52.1%; Pred. No. 0.34;
                                                                                     0;
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                                                                              Mismatches
                                                                79; Indels
                                                                                                                                     Length 1612;
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                                                                    Gaps
                                                                0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE
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                                                   misc_feature
                                                                                                                                                                                                                                                  source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Center project name: bA415J8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: humquery@sanger.ac.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Web site:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Center code: SC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matthews, N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  be preserved.
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                                                                                                             /clone="RP11-415J8"
                                                                                                                                                                   /db_xref="taxon:9606"
                                                                                                                                                                                                      /organism="Homo sapiens"
                                                                                                                                                                                                                                                                      Location/Qualifiers
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                                                                                                                                                                                                                                           .202682
                                               .53967

    Project Information
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138 CACCTCATAGGGAAGACAGGCCTGATCCTGGTGAGGGTTTGCCCA 94
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   258 CCCAAGAAGCACACGACCACCTGGGAAAGACAGGGGACAGTCTCCCAGCCTGGGCACCCT 199
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Summary Statistics
Assembly program: XGAP4; version 4.5
Sequencing vector: plasmid; 108752; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Consensus quality: 202251 bases at least 040
Consensus quality: 202335 bases at least Q30
Consensus quality: 202396 bases at least Q20
Insert size: 202482; sum-of-contigs
Insert size: 198528; 5.3% error; agarose-fp
Quality coverage: 10.24x in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            * NOTE: This is a 'working draft' sequence. It currently consists of 3 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. * This record will be updated with the finished sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (24-JAN-2002) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk On Feb 1, 2002 this sequence version replaced gi:17384473.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Center: Wellcome Trust Sanger Institute
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HOMO sapiens chromosome 1 clone RP11-415J8, *** SEQUENCING
PROGRESS ***, 3 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                    53968 54067: gap of 100 bp
54068 147217: contig of 93150 bp in length
147218 147317: gap of 100 bp
147318 202682: contig of 55365 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                 1 53967: contig of 53967 bp in length 54068 147217.
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/note="assembly_fragment:03338
fragment_chain:1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Norway rat.
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Stone, H., Sutton, A., Svatek, A.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    * NOTE: Estimated insert size may differ from sequence length

* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

* NOTE: This is a 'working draft' sequence. It currently

* consists of 75 contigs. The true order of the pieces

* is not known and their order in this sequence record is

* arbitrary. Gaps between the contigs are represented as

* runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (12-JAN-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission
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Center clone name: CH230-160H18
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Contact: hgsc-help@bcm.tmc.edu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Akhter, N., Ayele, K., Beckstrom-Sternberg, S.M., Benjamin, B., Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S., Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Haghighi, P., Ho, S.-L., Idol, J.R., Karlins, E., Laric, P., Lee-Lin, S.O., Legaspi, R., Maduro, Q.L., Maduro, V.B., Masiello, C., Mastrian, S.D., McCloskey, J.C., McDewell, J., Pearson, R., Prasad, A., Shevchenko, Y., Stantripop, S., Thomas, J.W., Thomas, P.J., Touchman, J.W., Tsurgeon, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L., Zhang, L.-H. and Green, E.D.
                                                                                                                                                                                                                                                                                                                                             Submitted (21-SEP-2001) NIH Intramural Sequencing Center, 8717 Grovemont Circle, Gaithersburg, MD 20877, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AC096681 145617 bp DNA linear HTG 21-Canis familiaris clone RP81-228C19, WORKING DRAFT SEQUENCE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        l Similarity 59.062; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                      Green, E.D.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.

1. (bases 1 to 145617)
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Canis familiaris
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AC096681
Summary Statistics

Sequencing vector: plasmid; n/a; 100% of reads

Sequencing vector: plasmid; n/a; 100% of reads

Chemistry: Dye-terminator Big Dye; 100% of reads

Assembly program: Phrap; version 0.990319

Consensus quality: 144648 bases at least Q40

Consensus quality: 144809 bases at least Q30

Consensus quality: 144809 bases at least Q20

Insert size: 145000; agarose-fp

Onality coverage: 10.18x in Q20 bases; agarose-fp

Quality coverage: 10.18x in Q20 bases; sum-of-contis
                                                                                                                                                                                                                                                                                                                                                                                                                                            (bases 1 to 145617)
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117006
117106
118474
118574
119787
119887
121197
121197
                                                                                                                                                                                                                Center project name: ci
Center clone name: 228C
                                                                                                                                                                                                                                                     Contact: nisc_mouse@nhgri.nih.gov
                                                                                                                                                                                                                                                                                                          Center: NIH Intramural Sequencing Center Center code: NISC
                                                                                                                                                                                                                                                                                      Web site: http://www.nisc.nih.gov
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121196:
121296:
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Pred. No. 1.2;
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of 1245 l
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of 1213
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of 1368
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     agarose-fp
sum-of-contigs
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NOTE: This is a 'working draft' sequence.

It currently

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REFERENCE
AUTHORS
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                                                                                                                          COMMENT
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                                                                                                                                                                                     JOURNAL
                                                                                                                                                                                                                              AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                misc_feature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            90 GGGGGGCAGGGGCGGGGGATGAGCCAGGGCCGAGAAGGAACT 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30 AGGAAGTCCCAGAAAGCACAGCTGACTTAGGGAAGGTCTGGGAAAAATCTCCCCTGCTTTT 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 148198 bp DNA linear HTG 07-HOMO Sapiens chromosome 11 clone RP11-223K12, WORKING DRAFT SEQUENCE, 9 unordered pieces.
                                                                                                                                             Submitted (28-FEB-2000) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. MO 63108, USA
  web site:http://genome.wustl.edu/gsc/index.shtml
------ Project Information ------
                                     Center: Washington University Genome Sequencing Center Center code: WUGSC
                                                                                                                   MO 63108, USA On Jun 14, 2000 this sequence version replaced gi:7715652
                                                                                                                                                                                                                          2 (bases 1 to 148198)
Waterston, R.H.
                                                                                                                                                                                                           Direct Submission
                                                                                                                                                                                                                                                                 Unpublished
                                                                                                                                                                                                                                                                                       The sequence of Homo sapiens clone
                                                                                                                                                                                                                                                                                                             Waterston, R.H.
                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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HTG; HTGS_PHASE1; HTGS_DRAFT.
                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                consists of 3 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence.
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1 28893 c 28921 g 43667 t
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clone_end:SP6
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/db_xref="taxon:9615"
/clone="RP81-228C19"
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                                                                                     ---- Genome Center ----
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Project Information
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Insert size: 151000; agarose-fp
Insert size: 147398; sum-of-contigs
Quality coverage: 4.53 in Q20 bases; agarose-fp
Quality coverage: 4.67 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Center project name: H_NH0223K12
------ Summary Statistics
Sequencing vector: M13; 1008
Sequencing vector: plasmid; 08
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85981
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116056
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12254
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12354
22568
22668
37703
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66694
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51154 .66693
                                                                                                                                                                                                                       vector_side:right"
66794. .85880
                                                                                                                                                                                                                                                                                                                                      /note="assembly_name:Contig7"
37703. .51053
                                                                                                                                                                                                                                                                                                                                                                                                                          2856. .12253
/note="assembly_name:Contig5"
                                                                                                                            vector_side:right"
                                                                                                                                                                                                                                                            /note="assembly_name:Contig9
clone_end:T7
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                                                                         /note="assembly_name:Contig12"
34635 c 33776 g 40404 t
                                                                                                              116056
                                                                                                                                                   clone_end:SP6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="assembly_name:Contig4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone="RP11-223K12"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                               /note="assembly_name:Contigl1
                                                                                                                                                                                                                                                                                                                                                                                         /note="assembly_name:Contig6"
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51053: contig
51153: gap of
66693: contig
66793: gap of
85880: contig
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12253:
12353:
 17.0%;
56.3%;
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                                                                                                                                                                                        .115955
                                                                                                                                                                                                                                                                                                                                                                             .37602
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 Score 35.8; D
Pred. No. 2.4;
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of 13351 bp in
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                     DB 2;
                                                                             806 others
                       Length 148198;
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All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       l (bases 1 to 176831)
Birren, B., Linton, L.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
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                                                                                      NOTE: This is a 'working draft' sequence. It currently consists of 2 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence.
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as soon as it is available and the accession number will
be preserved.
1 22120: contig of 22120 bp in length
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                                                                                                                                                                                                                                                                                                                                           Center project name: L10956
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Center: Whitehead Institute/ MIT Center for Genome Research Center code: WIBR
                                                                                                                                                                                                                                                                                                            Center clone name: 2010_I_16
                                                                                                                                                                                                                                                                                                                                                                                                Contact: sequence_submissions@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                  Web site: http://www-seq.wi.mit.edu
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      Maximum Match 100%
Listing first 45 summaries
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Copyright (c) 1993 - 2002 Compus
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/cgn2_6/ptodata/1/ina/5B_COMB.seq:*
/cgn2_6/ptodata/1/ina/6B_COMB.seq:*
/cgn2_6/ptodata/1/ina/6B_COMB.seq:*
/cgn2_6/ptodata/1/ina//BUTUS_COMB.seq:*
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Patent No. 5185262
Patent No. 5185262
Sequence 6, Appli
Sequence 14, Appl
Sequence 10, Appl
Sequence 10, Appl
Sequence 10, Appl
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      10, Appl
43, Appl
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RESULT 1 US-09-817-180-1

ALIGNMENTS

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; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 2674
; TYPE: DNA
; ORGANISM: Human
US-09-817-180-1
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; Sequence 1, Application US/09817180
; Patent No. 6340584
; GENERAL INFORMATION:
APPLICANT: GAN, Weiniu et al.
TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND
TITLE OF INVENTION: THEREOF
FILE REFERENCE: CL001183
; CURRENT APPLICATION NUMBER: US/09/817,180
; CURRENT FILING DATE: 2001-03-27
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                                                                                                                                             Sequence 5, Application PC/TUS9601735

SEQUENCE INFORMATION:

ENPELICANT: Marks, Andrew R.

TITLE OF INVENTION: HUMAN T CELL INOSITOL 1,4,5,-TRISPHOSPHATE
TITLE OF INVENTION: RECEPTOR

NUMBER OF SEQUENCES: 8

CORRESPONDENCE ADDRESS:

ADDRESSE: Brumbaugh, Graves, Donohue & Raymond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Loc
Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1083 CTCCGGAATGAAGAGGAGAACACCCCACCCCGGGAGCGGGTGCAGCTGCTGGGCAAGAGG 1142
ZIP: 10112-0228
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                       1143 CAAGTGCTGCAAGAAGCACTGCAGGGGCTGCAGGTAGCGCTGTGCAGCC 1191
                                                                                                                                                                                                                                                                                                                                                                                                                                                115 CAGGGCCGAGAAGGAACTCTGAAGACTCCGTAGATTGCTCTAGACCGCC 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity hes 59; Conserv
                                                                                STREET: 30 Rock
CITY: New York
STATE: NY
                                                              COUNTRY:
                                                                                                                               30 Rockefeller Plaza
                                                                USA
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54.1%;
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Pred. No. 2.2;
0; Mismatches
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SOFTWARE: FastSEQ Version 1.5 CURRENT APPLICATION DATA:

COMPUTER: IBM CON OPERATING SYSTEM:

IBM Compatible

DOS

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US-08-949-155-49/c

Sequence 49, Application US/08949155

Patent No. 6271436

GENERAL INFORMATION:
APPLICANT: Pledrahita, Jorge A
APPLICANT: Bazer, Fuller W
APPLICANT: Bazer, Fuller W
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LENGTH: 8791 base pairs
            ZIP: 77210-4433

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                            TITLE OF INVENTION: Compositions and methods for the TITLE OF INVENTION: Generation of Transgenic Animal Species NUMBER OF SEQUENCES: 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                              5551 AGTTATCGACCTCATCATGAAC 5572
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FRAGMENT TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: ci
HYPOTHETICAL: NO
ANTI-SENSE: NO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION: TELEPHONE: 212-408-2628
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APPLICATION NUMBER: 08/386,039
FILING DATE: 09-FEB-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  150 TGCTCTAGACCGCCTCAGACAC 171
APPLICATION NUMBER: US/08/949, 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        y Match 13.5%;
Local Similarity 50.0%;
                                                                                                                                                                                                STREET:
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                                                                                                                                            COUNTRY:
                                                                                                                                                                                                                  ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: nucleic acid
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REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
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                                                                                                                                                                             Houston
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                                                                                                                                            US
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Pred. No. 5.6;
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US-08-785-310A-4/c

Sequence 4, Application US/08785310A Patent No. 5840532

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                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/318,448
CURRENT FILING DATE: 1999-05-25
NUMBER OF SEQ ID NOS: 46
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 20
LENGTH: 3228
                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 20, Application US/09318448 Patent No. 6210950
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APPLICANT: Stenroos, Edward S.
TITLE OF INVENTION: METHODS FOR DIAGNOSING, PREVENTING, AND TREATING
TITLE OF INVENTION: DEVELOPMENTAL DISORDERS
FILE REFERENCE: 601-1-057
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                     LENGTH: 3228
TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (713) 789-2679
INFORMATION FOR SEQ ID NO: 4
SEQUENCE CHARACTERISTICS:
LENGTH: 4791 base pairs
1689 TGCCTGTGAAAGGGGGGTCCAGGAGCCCAGGCCCACAAGGAGCCCTGAGGCCTGTTGAGA 1630
                                 149 TTGCTCTAGACCGCCTCAGACACTCTCGGCGCAGCGTGGAGAG 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: TA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US 60
FILING DATE: 09-MAY-1997
ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 11-OCT-PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: Concurre CLASSIFICATION: 800 PRIOR APPLICATION DATA:
                                                                                                89 TGGGGGGGCAGGGGGGATGAGCCAGGGCCGAGAAGGAACTCTGAAGACTCCGTAGA 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        133 GTGAGGACTAGGGAGAATGAGCTTGGCATCCCCTCCCATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       133 CTGAAGACTCCGTAGATTGCTCTAGACCGCCTCAGACACT 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
les 56; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Hibler, David W. REGISTRATION NUMBER: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                        Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (512) 418-3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11-OCT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Concurrently Herewith
                                                                                                                                                      13.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13.3%;
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 Mismatches

                                                                                                                                                    Score 27.8; DB 4; Pred. No. 6.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TAMK: 177
                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 4; Length 4791;
5.1;
                                                                                                                                    47;
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                                                                                                                                                                  Length 3228;
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                                                                                                                                 Gaps
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5185262-2
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                                                                                                                                                                                                                                                                          APPLICANT: KOHAMA, KEIKO; KOBAYASHI, MIKI; KURUSU, YASUROU; YUKAMA, HIDEAKI; FUKUSHIMA, MAKIKO
TITLE OF INVENTION: DNA FRAGMENT CONTAINING GENE WHICH ENCODES THE FUNCTION OF STABILIZING PLASMID IN HOST MICROORGANISM NUMBER OF SEQUENCES: 2
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                      ; Patent No. 5185262
                                                                                                                        5185262-2
                                                                                                                                                          :SEQ ID NO:2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (415) 343-4342
INFORMATION FOR SEQ ID NO: 4:
                                          Matches
                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: McKnight, Steven L.
APPLICANT: Russell, David W.
TITLE OF INVENTION: Neuronal PAS Domain Protein
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: UT TELECOMMUNICATION INFORMATION: TELEPHONE: (415) 343-4341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 4184 base pair
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear MOLECULE TYPE: cDNA
                                                                                                                                                                       APPLICATION NUMBER: US/07/c
FILING DATE: 01-FEB-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 385,414
FILING DATE: 26-JUL-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: 268 BUSH STREET, SUITE 3200 CITY: SAN FRANCISCO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       171 GCTTCTGTCCGGGCACGCAGTACCCCTCTAGCACCCTCGGAGGACCCCCGA 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              138 GACTCCGTAGATTGCTCTAGACCGCCTCAGACACTCTCGGCGCAGCGTGGA 188
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       231 CTCCCTACGCTTCGGGATGCCTGCGGTGGGGCTCTGGAAGGGCAGCGGGCAATCTTGAAA 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/785,310A FILING DATE: 21-JAN-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           78 CTCCCTGCTTTTGGGGGGGCAGGGGGGGGGGGGGTGAGCAGGGAGGAACTCTGAA 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local
80 CCCTGCTTTTGGGGGGGGGGGGGGGGGGGGGGGCCGAGGAGGGAACTCTGAAGA 139
                                                                                                                                       ENGTH: 1762
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      59;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    h 13.2%; Score 27.8; DB 2; Length 4184; Similarity 53.2%; Pred. No. 6.7; 59; Conservative 0; Mismatches 52; Indels 0
                                             60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             nucleic acid
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                                          Conservative
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                                             12.9%; score 27; DB 6; Length 1/o. 52.2%; Pred. No. 8.9; ative 0; Mismatches 55; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                36,627
                                                                                                                                                                                                                                                                   US/07/473,396
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                                                                                     DB 6; Length 1762;
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APPLICANT: KOHAMA, KEIKO;KOBAYASHI, MIKI;KURUSU, YASUROU;
YUKAWA, HIDEAKI;FUKUSHIMA, MAKIKO
TITLE OF INVENTION: DNA FRAGMENT CONTAINING GENE WHICH
ENCODES THE FUNCTION OF STABILIZING PLASMID IN HOST MICROORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5185262-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5185262-
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                                                                                                                             , LUCATION: (1)...(3740); OTHER INFORMATION: n = A,T,C or G US-09-162-274A-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; GENERAL INFORMATION:
 밁
                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/162,274A
CURRENT FILING DATE: 1999-09-29
NUMBER OF SEQ ID NOS: 6
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 6
LENGTH: 3740
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 6, Application US/09162274A Patent No. 6316188
                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Liggett, Stephen B.
APPLICANT: Galinsky, Raymond E.
APPLICANT: Weinshilboum, Richard M.
                                                                         Matches
                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Lachman, Herb M. TITLE OF INVENTION: HISTAMIN FILE REFERENCE: 07039/080001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 01-FEB-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 385,414
FILING DATE: 26-JUL-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  140 CTCCGTAGATTGCTCTAGACCGCCTCAGACACTCTCGGCGCAGCGTGGAGAGGAT 194
                                                                                                                                                                                                                                    ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          213 CTCGATAGCTATTCCTCGACAGCTCGAGCGCATTACCTCCTTGCTAGCTGATGAT 267
                                                                                                                                                                                                                     FEATURE:
                                                                                                                                                                                                                                                        TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           140 CTCCGTAGATTGCTCTAGACCGCCTCAGACACTCTCGGCGCAGCGTGGAGAGGAT 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      214 CTCGATAGCTATTCCTCGACAGCTCGAGCGCATTACCTCCTTGCTAGCTGATGAT 268
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APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 1763
                                  24 CTGTCAAGGAAGTCCCAGAAAGCACAGCTGACTTAGGGAAAGGTCTGGGAAAAATCTCCCT 83
                                                              12.8%;
Local Similarity 53.9%;
es 55; Conservation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       60;
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                                                                               0;
                                                                           Score 26.8; DB 4; Length 3740; Pred. No. 14; 0; Mismatches 47; Indels 0
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US-09-328-111-83
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 14, Application US/08232463 Patent No. 5670367
                                                      1061 AAGCTCCCTCGACCTGCAGCCAAGCTCGG 1033
                                                                                                               GENERAL INFORMATION:
APPLICANT: DORNER, F.
APPLICANT: SCHEIFLING
                                                                                                                                                                              TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
TELEPAX: (703)683-4109
                                                                                                                                                                                                                                                                                                                                                             IMMEDIATE SOURCE:
                                                                                    149 TTGCTCTAGACCGCCTCAGACACTCTCGG 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: EP 91
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, V
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 22313
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
FILING DATE:
                                                                                                                                               89 TGGGGGGGCAGGGGCGGGGATGAGCCAGGGCCGAGAAGGAACTCTGAAGACTCCGTAGA 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                              29 AAGGAAGTCCCAGAAAGCACAGCTGACTTAGGGAAAGGTCTGGGAAAAATCTCCCTGCTTT 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKNER, F.G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
NUMBER OF SEQUENCES: 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3227 GGTTGGAGAGATTAGGGGTGGGGAGTGGATGAAGGGCCCAGA 3186
                                                                                                                                                                                                                                                              Local Similarity
nes 17; Conserv
                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                               CLONE:
                                                                                                                                                                                                                                                                                                                                                                                                                              ENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: USA
ZIP: 22313-0299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  84 GCTTTTGGGGGGGCAGGGGGGGGGATGAGCCAGGGCCGAGA 125
                                                                                                                                                                                                                                                                                                                                                                                         nucleic acid
DEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  899149
                                                                                                                                                                                                                                                                                                                                           PTZgpt-F1s
                                                                                                                                                                                                                                                                                                                                                                                                                         7218 base pairs
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                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3: Foley & Lardner
1800 Diagonal Road, Suite 500
                                                                                                                                                                                                                                                                                                                                                                         linear
                                                                                                                                                                                                                                              12.7%; Score 26.6; DB 1; Length 7218; 11.4%; Pred. No. 21; ative 74; Mismatches 58; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EP 91 114 300.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       29,768
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                                                                                                                    ; NAME/KEY: CDS
; LOCATION: (47)...(1489)
US-09-487-445-10
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                                                      Matches 51;
                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                     SEQ ID NO 10
LENGTH: 1489
                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 10, Application US/09487445 Patent No. 6258600
                                                                                                                                                                                                                                                                                                           APPLICANT: Hong Zhang
APPLICANT: Lex M. Cowsert
TITLE OF INVENTION: ANTISENSE MODULATION OF CASPASE 8 EXPRESSION
FILE REFERENCE: RTS-0107
                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/09/487,445
CURRENT FILING DATE: 2000-01-19
NUMBER OF SEQ ID NOS: 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQ ID NO 83
                                                                                                                                                                                   ORGANISM: Mus musculus FEATURE:
                                                                                                                                                                                                                      TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: FORG, DONNA M.
APPLICANT: Lewis, Marcia E.
APPLICANT: Lewis, Marcia E.
APPLICANT: Monahan, John E.
APPLICANT: Schlegel, Robert
TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION
TITLE OF INVENTION: PRODUCTS
FILE REFERENCE: CCD-257 (US)
CURRENT APPLICATION NUMBER: US/09/328,111
CURRENT APPLICATION NUMBER: US/09/328,111
CURRENT FILING DATE: 1999-06-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EARLIER APPLICATION NUMBER: US 60/088,801
EARLIER FILING DATE: 1998-06-10
NUMBER OF SEQ ID NOS: 850
SOFTWARE: FastSEQ for Windows Version 3.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 83, Application US/09328111 Patent No. 6262333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:

NAME/KEY: misc_feature
LOCATION: (1)...(584)
OTHER INFORMATION: n = A,T,C or G
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TYPE: DNA
ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 175 CGGCGCAGCGTGGAGAGGATTTGT 198
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         486 GGGGCCAACATGCATTGGCTTTGT 509
5 CTTGTTCTTCTCCTCAGCCTGTCAAGGAAGTCCCAGAAAGCACAGCTGACTTAGGGAAG 64
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Similarity 57.1%;
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Catino, Theodore J.
                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Burgess, Christopher C.
Bushnell, Steven E.
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                                                          12.6%; Score 26.4; DB 4; Length 1489; 55.4%; Pred. No. 13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0,
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Pred. No. 9.2;
                                        Mismatches 41; Indels
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                                                                                                                                 US-08-257-963B-10
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                                                                Matches
                                                                                                Query Match
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   6869
                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: 20
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 514
PRIOR APPLICATION UNBER: 07/952,796
FILING DATE: 24-SEPT-1992
ATTORNEY/AGENT INFORMATION:
NAME: DOROTHY R. AUTH
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MEDIUM TYPE: Floppy Disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1114
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 7210 Base Pair
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                             MOLECULE TYPE:
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                                                                                                                                                                                                                                FEATURE:
                                                                                                                                                                                                                                                              IMMEDIATE SOURCE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  65
                                                                                                                                             OTHER INFORMATION: 7.2 kb No. 5840686 1 fragments
OTHER INFORMATION: Derived from human placental genomic DNA
                                22 GCCTGTCAAGGAAGTCCCAGAAAGCACAGCTGACTTAGGGAAGGTCTGGGAAAAATCTCC 81
                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
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                                                                                  Local Similarity
                                                                                                                                                                             IDENTIFICATION METHOD:
                                                                                                                                                                                                               NAME/KEY: JT106
                                                                                                                                                                                                                                                                               ORGANISM:
                                                                                                                                                                                                                                                                                                                            TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                         TYPE: Nucleic Acid
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                                                                                                                                                                                                                                               LIBRARY: DASH II
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                                                                                                                                                                                                                                                                                                                                                                            7210 Base Pairs
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Taniwaki, Takayuki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      USA
                                                                                                                                                                                                                                                                                                                                                                                                                           (212)
                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chader, Gerald J.; Becerra, S.
                                                                                                                                                                                                                                                                                                                            Unknown
                                                                                                                                                                                                                                                                             Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Morgan & Finnegan
                                                                                                                                                                                                                                                                                                            Genomic DNA
                                                                                                                                                                                                                                                                                                                                            Double
                                                                                                                                                                                                                                                                                                                                                                                                                         751-6849
                                                                                12.5%;
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                                                                                Score 26.2;
Pred. No. 28;
                                                                 Mismatches
                                                                                                DB
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                                                                                                                        Best
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                                                                                              Matches
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INFORMATION FOR SEQ ID NO:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: WORDPERFECT 5.1 CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 24-SEP-1992 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: 08/2: FILING DATE: 07-JUN-1994 PRIOR APPLICATION DATA: APPLICATION NUMBER: 07/9: APPLICATION NUMBER: 08/2: APPLICATION NUMBER: 07/9: APPLICATION NUMBER: 0
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                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE:
NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE:
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                                                                                                                                                                                                                                                 IDENTIFICATION METHOD:
OTHER INFORMATION: 7.
OTHER INFORMATION: fr
OTHER INFORMATION: ge
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                             22 GCCTGTCAAGGAAGTCCCAGAAAGCACAGCTGACTTAGGGAAGGTCTGGGAAAAATCTCC 81
                                                                                                                        Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LIBRARY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REGISTRATION NUMBER:
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                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                              JT6A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Genomic DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Double
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                                                                                                                        12.5%;
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DERIVED FACTOR: CHARACTERIZATION
ORGANIZATION AND SEQUENCE OF THE
                                                                                                                                                                                                                                           7.0 kb No. 6319687 1-No. 6319687 fragment; Derived from human placental genomic DNA; also referred to as JT106
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                                                                                                                        Score 26.2;
Pred. No. 28;
                                                                                              Mismatches
                                                                                                                                                      DB 4;
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                                                                                           48;
                                                                                                                                                         Length 7210;
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   Matches
                                Query Match
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NFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Chader, Gerald J.; Becerra, Sofia APPLICANT: Patricia; Schwartz, Joan P.; APPLICANT: Taniwaki, Takayuki
                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 7210 Base Pairs
                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 20
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/9:
FILING DATE: 24-SEP-1992
ATTORNEY/AGENT INFORMATION:
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TITLE OF INVENTION:
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                                                                                                                                                                                                                                              ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 30-DEC-PRIOR APPLICATION DATA:
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PRIOR APPLICATION NIMBER: 08/367,841
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
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                                                                                                                                                                                  FEATURE:
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                                                                                                                                                                                                                                                                MOLECULE TYPE:
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                  Local
                                                                               OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                  APPLICATION NUMBER: 08/3 FILING DATE: 30-DEC-1994
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                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: DOROTHY R. AUTH REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: 08/2 FILING DATE: 07-JUN-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC Compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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STREET: 345 Park Avenue
                                                                                                                                                  NAME/KEY: JT6A
LOCATION:
                                                                                                                                                                                                                                   ORGANISM:
                                                                                                                                                                                                                                                                                               TYPE: Nucleic Acid
STRANDEDNESS: Doub
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   55;
                 Similarity
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   Conservative
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DERIVED FACTOR: CHARACTERIZATION
ORGANIZATION AND SEQUENCE OF THE
               12.5%;
                                                                               fragment; Derived from human placental genomic DNA; also referred to as JT106
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               Score 26.2;
Pred. No. 28;
Mismatches
                                DB 5;
 48;
                              Length 7210;
 Indels
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                                                                Matches
                                                                               Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 43,
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APPLICATION NUMBER: US/
FILING DATE: 30-DEC-199/
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
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APPLICANT:
 6861 GGCACTCCAGGGAGCAGAAAAGAGGGGTGCAAGGGAGAGGAAATGCGGAGACAGCAGCCC 6920
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: 08/2: FILING DATE: 07-JUN-1994 PRIOR APPLICATION DATA: APPLICATION NUMBER: 07/9:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6929 CTGCAATTTGGGCAAAAGGGTGAGTGGATGAGAGAGGGCAGAG 6971
                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION: TELEPHONE: (212) 758-4800
                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 24-SEP-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                FEATURE:
                                                                                                                                                                                                                                                 MOLECULE TYPE:
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                                                                                                                                           OTHER INFORMATION: full length g
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CITY: New York
                              22 GCCTGTCAAGGAAGTCCCCAGAAAGCACAGCTGACTTAGGGAAGGTCTGGGAAAAATCTCC 81
                                                                                                                                                                                                                                                               STRANDEDNESS:
TOPOLOGY: Unl
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OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                             LOCATION:
IDENTIFICATION METHOD:
                                                                                                                                                                                                                 NAME/KEY: P1-147
                                                                                                                                                                                                                                                                                                 TYPE:
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                                                                                                                                                                                                                                                                                                              22481 Base Pairs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           345 Park Avenue
                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                 (212)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chader, Gerald J.; Rodriguez, Ignacio R.; Mazuruk, Krzysztof;
                                                                                                                                                                                                                                                                Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WORDPERFECT 5.1
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                                                                               12.5%;
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DERIVED FACTOR: CHARACTERIZATION GENOMIC
ORGANIZATION AND SEQUENCE OF THE PEDF GENE
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                                                                                                                                                          full length genomic
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                                                                              Score 26.2;
Pred. No. 44;
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                                                                Mismatches
                                                                                                                                              PEDF plus flanking sequences
                                                                                             DB 4;
                                                                48;
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Search completed: November 6, 2002, 14:20:31 Job time: 42.9733 secs

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Post-processing: Minimum Match 0%
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                                                                                                                                                              Score
  32.8
32.8
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  13736207 seqs, 6748477542 residues
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Copyright (c) 1993 - 2002
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gb_est2:*
gb_htc:*
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  772
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           CNS01TZC
BE336705
BI828928
BG035198
BF759824
AQ898422
                                                                                BI256085
AG076601
                                                               BF172864
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Compugen Ltd.
BG855275 1024042C0
BG479234 602526449
AA690752 vu57c08.r
BG775847 602716308
B1256085 602978917
AG076601 Pan trog1
B181409 603074508
BF172864 MYE0121 M
AL167169 Tetraodon
BE336705 ba9901.y
B1828928 603075090
BC035198 603234706
BF759824 PM0-CT064
AQ889422 HS_3135_B
AL108399 Drosophil
                                                                                                                                 AZ971837 2M0245B02
AU119486 AU119486
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519	305	777	755	750	707	687	674	574	567	502	464	461	447	428	413	412	411	407	380	377	356	334	300	288	1019	490	430	
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AU175395	AA153765	в1463395	AG002169	AG002170	AG002182	AG002187	AG002186	BI438774	AA543126	AA779225	AI201132	AI184928	AI804686	BM127990	AW169135	BM127741	AW473156	AI874207	AW439335	AA776500	BF195077	BF001888	AW517011	AA788598	rn.	AI561790	BB776545	
AU175395 AU175395	AA153765 mr04b03.r	BI463395 603204431	AG002169 Homo sapi	AG002170 Homo sapi	AG002182 Homo sapi	AG002187 Homo sapi	AG002186 Homo sapi	BI438774 1c26e06.x	AA543126 vk36b12.r	AA779225 zj39e07.s	AI201132 qf64f09.x	AI184928 ck28c02.x	AI804686 tt94e04.x	вм127990 if08c08.у	tj19a09.	BM127741 if08c08.x	AW473156 xy14h02.x	AI874207 wm50c02.x	:t17g05.	AA776500 ahllf10.s	BF195077 7o94f04.x	BF001888 7g94h12.x	AW517011 xp90c11.x	AA788598 ag58g10.s	AL343657 Tetraodon	AI561790 vv66b12.x	BB776545 BB776545	

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## ALIGNMENTS

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SOURCE
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AZ971837/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                        JOURNAL
                                                                                                    source
                                                                                                                                                            Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu
Insert Length: 1000 Std Error: 0.1

Plate: 0245 row: B column: 02

Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      689 bp DNA linear GSS 27-APR-200245B02R Mouse 10kb plasmid UUGC2M library Mus musculus genomic clone UUGC2M0245B02 R, DNA sequence.
                                                                                                                                                                                                                                                                                                                       University of Utah (
University of Utah
Rm. 308, Biomedical
                                                                                                                                                                                                                                                                                                                                                                                 Unpublished (2000)
Contact: Robert B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 689)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
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                                                                                                                    quality sequence stop: 689
Location/Qualifiers
                                                                                                                                                                                                                                                                                                        USA
                                       /organism="Mus musculus"
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/db_xref="taxon:10090"
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/clone_lib="Mouse 10kb plasmid UUGC2M library"
                                                                                                                                                                                                                                                                                                                                                                Genome Center
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137 GTCTTGCTTTTTCTTCTGGGCTTGCTGAGGAAGTCCCAGGCAGCGTAGACGTCTTGGGGG 78
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    62 AAGGTCTGGGAAAAATCTCCCTGCTTTTGGGGGGGGCAGGGGCGGGGGATGAGCCAGGGCC 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
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                                                                                                  Email: genomics@hri.co.jp
HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix
Research Institute; cDNA library construction: Department of
Virology, Institute of Medical Science, University of Tokyo, and
Helix Research Institute.
                                                                                                                                                                                                                                                                           Genomics Laboratory
Helix Research Institute
1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
Tel: 81-438-52-3951
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 (bases 1 to 772)
1 (bases 1 to 772)
Ota,T., Nishikawa,T., Suzuki,Y., Ishii,S., Saito,K., Kawai,Y., Ota,T., Nishikawa,T., Suzuki,Y., Nagai,T., Sugano,S. and
                                                                                                                                                                                                                                                                                                                                                                                            Contact: Takao Isogai
                                                                                                                                                                                                                                                                                                                                                                                                                                                  HRI human cDNA project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwD42 (gi|4732114(gb|AF129072.1), a copp-number inducible derivative of plasmid Rl. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XLIO-Gold (Stratagene) cells and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The
              /organism="Homo sapiens"
                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        adaptored DNA was purified and size-selected for a 9.5 to
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/note="Vector: PWD42nv; Purified genomic DNA from M.
/note="Vector: PWD42nv; Purified genomic DNA from M.
/note="Vector: PWD42nv; Purified genomic DNA from the Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Laboratory Mouse DNA Resource
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68.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            198 TAAATCTGGAGGAAGCTCTTGCCTGGGGGAACATTACAGAGCCTGGAGCATAGGTTA 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   157 GACCGCCTCAGACACTCTCGGCGCAGCGTGGAGAGGATTTGTGCA 201
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Grossman,A., Davies,J., Federspiel,N., Harris,E., Lefebvre,P., McDermott,J.P., Sliflow,C., Stern,D. and Surzycki,R. Analyses of the Chlamydomonas reinhardtil Genome: A Model, Unicellular System for Analyzing Gene Function and Regulation in Vascular Plants; project phase 2 Unpublished (2000)
Contact: Charles Hauser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chlamydomonas reinhardtii.
Chlamydomonas reinhardtii
Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Duke University
Durham, NC 27708-1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Charles Hauser DCMB Box 91000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BG855275 939 bp mRNA linear EST 29-MAY-; 1024042C07.yl C. reinhardtii CC-1690, normalized, Lambda Zap II CC-16mydomonas reinhardtii cDNA, mRNA sequence.
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919 613 8177
XhoI; This library, constructed by John Davies and Jeffrey McDermott, combines cDNAs from CC-1690 cells grown to mid-log phase in TAP (acetate-containing) medium in the light, TAP medium in the dark, HS (minimal) medium in ambient levels of CO2 and HS medium bubbled with 5% CO2. PolyA mRNA was purified from each sample, pooled and cDNA synthesized. The cDNA was directionally cloned into lambda ZAP II (Stratagene) in the EcoRI (5') and XhoI (3') sites. PBluescript II SK-plasmids were excised from the lambda ZAP clones by superinfection with ExAssist (Stratagene) phage. The library was normalized using method 4 described in Bonaldo et al (1996) Genome Research 6: 791-806."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     chauser@duke.edu
              ø
                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Chlamydomonas reinhardtii"
/strain="CC-1690 wild type mt+ 21gr"
/db_xref="taxon:3055"
/clone_lib="C. reinhardtii CC-1690, normalized, Lambda Zap
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/note="vector: pys185FL3
170 t 3 other
                                                                                                                                                                                                                                                                                                                                                                                         /note="Vector: pBluescript II SK-; Site_1: EcoRI; Site_2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   576 GAAGGTTCACAGAACGTGGCGAGTGGGGAAGAACAGGTAACGCGGTTATGGGGAAGCGAGG 517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   516 GGGGGGGGGGGGGGAGGGAACGGGAATGAAGGCAGAGGAAACGGGTGAAAAGGATAGA 459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Match 16.6%;
Local Similarity 55.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 source
                                                       114 CCAGGGCCGAGAAGGAACTCTGAAGACTCCGTAGATTGCTCTAGACCGCCTCAGACACTC 173
                                                                                                               427 AATTGGCAAAGCTGTGGAAGACTCCACAGCCCTACTGGGAGGCACGGAGGGTGGCGAGG 486
487 CCAGGCTCAGCTGGAAGCTCAGAAAGCCCCACGCAGGACTTCCAGAGGGCCACAGAGGTGC 546
                                                                                                                                                                       Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           602526449F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:4649772 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BG479234.1 GI:13411513
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov plate: LLCM1430 row: b column: 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   High quality sequence stop: 681.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cDNA Library Preparation: Ling Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. clone distribution: MGC clone distribution information can be
                                                                                                                                                                                                                                                                    Similarity
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//clone="IMAGE:4649772"
//clone="IMAGE:4649772"
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//tissue_type="choriocarcinoma"
//tissue_type="choriocarcinoma"
//lab.host="DH10B (phage-resistant)"
//lab.host="DH10B (phage-resistant)"
//lab.host="DH10B (phage-resistant)"
//ote="Organ: placenta: Vector: pOTB7: Site_1: XhoI;
//ote="Organ: placenta: potB7: Site_1: XhoI;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  174 TCGGCGCAGCGTGGAGAGGATTT 196
                                                                          105 GGGGATGAGCCAGGGCCGAGAAGGAACTCTGAAGACTCCGTAGATTGCTCTAGA 158
                                                                                                                                                        Match 16.2%;
Local Similarity 56.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 623)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BTEB ; , mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Marra M/Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Waterston, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    house mouse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        High quality sequence stop: 377.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    possible reversed clone: similarity on wrong strand seq primer: -28m13 rev2 ET from Amersham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: mouseest@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WashU-HHMI Mouse EST Project
                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="Organ: mammary gland: Vector: pT7T3D-Pac (Pharmacia ) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. RNA provided by Dr. Minoru Ko, Wayne State Univ. Library constructed and normalized by Bento Soares and M.Fatima
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /tissue_type="mammary gland"
/dev_stage="4 weeks"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone_lib="Soares_mammary_gland_NbMMG"
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                                                                                                                                                                                                                                                                               828 GGAACTGGGCGGCATGGAGGCGGCGCCACGGAGGGCCAAAGCGGACNCCG 877
                                                                                                                                                                                                                                                                                                                                                          768 GTGCCTGGAACCACAGCTGGCCTGGACCAGGACAGTGAAGCAATAACCTGGAGCTAGGGC 827
                                                                                                                                                                                                                                                                                                                        95 GGCAGGGGGGGGGTGAGGCCAGGGCCGAGAAGGAACTCTGAAGACTCCG 144
                                                                                                                                                                                                                                                                                                                                                                                     35 GTCCCAGAAAGCACAGCTGACTTAGGGAAGGTCTGGGAAAAATCTCCCCTGCTTTTGGGGG 94
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                                                                                                                                      BI256085
602978917F1 NCI_CGAP_Li9 Mus musculus cDNA clone IMAGE:5123621 5',
                                                             house mouse
                                                                                    BI256085.1 GI:14810144
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Plate: LLCM1707 row: o column: 02 High quality sequence stop: 816.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tissue Procurement: Louis M. Staudt, M.D., Ph.D. CDNA Library Preparation: Ling Hong/Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MCC clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            http://image.llnl.gov
Plate: LLCM1707 row:
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National Institutes of Health, Mammalian Gene Collection (MGC)
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Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 895)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /tissue_type="primary B-cells from tonsils (cell line)"
/lab_host="DHIOB (phage-resistant)"
/note="Organ: B-cells; Vector: pOTB7; Site_1: Xhor;
Site_2: EcoR1; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/Xhor sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit Note: this is a NIH_MGC Library." (Life Technologies).

77 a 284 c 292 g 141 t 1 others
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/clone_lib="NIH_MGC_48"
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/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local
Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical
                      Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y. Direct Submission
                                                                                                                                                             Fujiyama,A., Hattori,M., Toyoda,A.,
Totoki,Y., Watanabe,H. and Sakaki,Y.
                                                                                                                                 Unpublished
                                                                                                                                                        BAC end
                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan
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Pan troglodytes maie lymphoblast DNA, clone_lib:PTB Chimpanzee Male
BAC Library clone:PTB-070N17.F.
                                                                                                                                                                                                                                                                            Pan troglodytes
                                                                                                                                                                                                                                                                                                                                                 AG076601.1 GI:16628403
GSS; GSS (genome survey
                                                                                                                                                                                                                                                                                                                                                                                   Pan troglodytes DNA, clone: PTB-070N17.F, genomic survey sequence.
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Similarity 53.9%; Score 33.6; D
Similarity 53.9%; Pred. No. 33;
69; Conservative 0; Mismatches
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cDNA Library Arrayed by: Incyte Genomics, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
plate: LLAM11302 row: b column: 06
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Tissue Procurement: ATCC
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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/organism="Mus musculus"
/db_xref="taxon:10090"
/db_xref="taxon:10090"
/clone="IMAGE:5123621"
/clone="IMAGE:5123621"
/clone="IMAGE:5123621"
/clone="IMAGE:5123621"
/clone="IMAGE:5123621"
/clone="IMAGE:5123621"
/clone="IMAGE:5123621"
/clone="INGI_CGAP_Li9"
/lab_host="Organ: liver: Vector: pcMv-SpORP6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally Primer: Oligo dT. Site_2: SalI; Cloned unidirectionally Primer: Oligo dT. Average insert size 1.9 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."

48 a 223 c 187 g 137 t
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                                                                                                                                                                                                   Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
                                                                                                             Plate: LLAM11413 row: p column:
                                                                                                                   DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
                                                                                                                                                                                                                                                                                  Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                              1 (bases 1 to 258)
NHH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            78;
                                                                                            High quality sequence stop: 258.
                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                603074508F1 NIH_MGC_119 Homo sapiens cDNA clone IMAGE:5166577 5',
                                                                                                                                                                                                                                                                                                            Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        mRNA sequence.
BI831409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BI831409.1 GI:15942959
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:chimpbes@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170)
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R.Site 2 : SacI.
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/clone="IMAGE:5166577"
                /db_xref="taxon:9606"
                                /organism="Homo sapiens"
                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /cell_type="lymphoblast"
/clone_lib="PTB Chimpanzee Male BAC Library"
178 c 237 g 261 t 15 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Pan troglodytes"
/db_xref="taxon:9598"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone="PTB-070N17.F"
/sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
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BF172864
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                                                                                                                                                                                                                                                                                                                                                                                           FORWARD: 5'-GCCAAGCTCGAAATTAACCCTCACTAAAGGG-3'
BACKWARD: 5'-CCAGTGAATTGTAATACGACTCACTATAGGGCG-3'
Seq primer: 5'-GAAATTAACCCTCACTAAAGG-3'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              University Health Network 610 University Ave., 5-126, Toronto, Ontario, M5G 2M9, Canada Tel: (416) 946-4639 Fax: (416) 946-6546
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The transcriptional phenotype of myeloma cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: A. Keith Stewart, M.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claudio, J.O., Tang, H., Khan, E.M., Voralia, M., Li, Z., Cukerman, E., Franciso-Pabalan, O., Liew, C.C. and Stewart, A.K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claudio, J.O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 303)
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BF172864
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        k.stewart@utoronto.ca
Note "Vector: Lambda Zap Express; Site_1: EcoRI; Site_2: XhoI; Myeloma cells from multiple myeloma pattents' bone marrow were purified by magnetic cell sorting. mRNA were purified and an oligo d(T)18 primer containing XhoI restriction site was used to prime first strand synthesis using M-MLV reverse transcriptase. To protect the cDNAs from XhoI digestion in subsequent cloning step, the nucleotide analogue 5-methyl-dCTP was added to the
                                                                                                                                                                                    /tissue_type="Blood"
/cell_type="myeloma"
/cev_stage="multiple_myeloma"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Note="Organ: brain; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA source normal medulla from anonymous male age 27. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.3 kb, insert size range 0.9-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 013. Note: this is a NHIMGC Library."
                                                                                                                                                                                                                                                              /sex="male"
                                                                                                                                                                                                                                                                                 /clone_lib="Myeloma (MYE) cDNA library"
                                                                                                                                                                                                                                                                                                            /db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                 ∕organism="Homo sapiens"
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/lab_host="DH10B"
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67.1%;
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Pred. No. 31;
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RESULT 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GSS; genome survey sequence 
Tetraodon nigroviridis.
                                                                                                                                                                                                                                Submitted (12-APR-2000) to the EMBL/GenBank/DDBJ databases This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tetraodon nigroviridis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished
2 (bases 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Roest-Crollius, H., Jaillon, O., Dasilva, C., Fizames, C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tetraodontidae; Tet: 1 (bases 1 to 545)
                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Charaterization and repeat analysis of the compact genome of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Weissenbach,J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bouneau, L., Billault, A., Quetier, F., Saurin, W., Bernot, A. and
                                                                                                                                                                                                                                                                                                                                                                        Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tetraodon nigroviridis DNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human gene number estimate provided by genome wide analysis using
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       freshwater pufferfish Tetraodon nigroviridis
                                                                                                                                                                                                                                                                                                                                                                                                                       (bases 1 to 545)
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        139
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                              PUC-Ori"
                                                                                                       /organism="Tetraodon nigroviridis"
/db_xref="taxon:99883"
/clone="195P21"
                                                      /clone_lib="G"
/note="Genoscope sequence ID : COAG195CH11SP1~end
                                                                                                                                                                                                          Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              300 TGCCSGAGACGCCCVMAGAAACCCBCAGAG 329
                                                                                                                                             90 GGGGGGCAGGGGGGGGGATGAGCCCAGGGCCGAGAAGGAACTCTGAAGACTCCGTAGAT 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
                                                                        119 GCCGAGAAGG 128
299 GCCGGGAAGG
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                                                                                                                                                                                                                                                                                                                                Local Similarity
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                                                                                                                                                                                                                                                                                              47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished (1999)
Other_ESTs: ba99d01.x1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 597) NIH-MGC http://mgo.nci.nih.gov/. National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cDNA Library Preparation: Ling Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov/image/html/iresources.shtml
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: cgapbs-remail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Robert Strausberg, Ph.D.
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/Clone_Tibe"NIH_MGC_14"
/tissue_type="renal cell adenocarcinoma"
/lab_host="pH10B (phage-resistant)"
/note="organ: kidney; Vector: pOTB7; Site_1: XhoI; Site_2:
/note="organ: kidney; Vector: pOTB7; Site_1: XhoI; Site_2:
/total cell adenocarcinoma"
/total cell adenocarcinoma
/total cell adenoca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubhn (University Of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."

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/clone="IMAGE:2958049"
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Pred. No. 39;

 Mismatches

                                                                                                                                                                                                                                                                                                                                Score 33.2;
Pred. No. 40;
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                                                                                                                                                                                                                                                                 GCCGGGAAGG 544
                                                                                                                               602324706F1 NIH_MGC_90 Homo sapiens cDNA clone IMAGE:4413048
                                                                                                                                                                                                                                                                                                                                                                                                                       47;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                              Homo sapiens
                                                                                                           BG035198
                                                                                                                         mRNA sequence.
                                                                                                                                                                    BG035198
                                                                                     BG035198.1 GI:12429091
                                                    human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tissue Procurement: Life Technologies, Inc. cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               High quality sequence stop: 662.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov http://image.llnl.gov d column: 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: cgapbs-r@mail.nih.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NATH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished (1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cloning). Average insert size 1.3 kb, insert size range 0.9-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="Organ: brain; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA source normal medulla from anonymous male age 27. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              this is a NIH_MGC Library."
1 227 c 203 g 121 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /tissue_type="medulla"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone="IMAGE:5166694"
/clone_lib="NIH_MGC_119"
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67.1%;
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Pred. No. 4
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COMMENT
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BF759824
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Best Local Similarity
Matches 47; Conserv
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                                                                                                                                                             JOURNAL
                                                                                                                                                                                                        TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM
                                                                                                                                                                                                                                                                                                                                           AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AUTHORS
TITLE
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                                Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                          Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
                                                                                                       Contact: Simpson A.J.G.
                                                                                                                                                                                sequence tags
                                                                                                                                                                                       Shotgun sequencing of the human transcriptome with ORF expressed
                                                                                                                                                                                                                                    1 (bases 1 to 386)
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
                                                                                                                                                                                                                      Simpson, A.J
                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
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BF759824.1 GI:12107724
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cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
http://image.llnl.gov k column: 01
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Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished (1999)
+55-11-2704922
                                                                                                                                               Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
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/tissue_type="adenocarcinoma, cell line"
/lab_host="DH108 (phage-resistant)"
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Site_2: SalI; Cloned unidirectionally; oligo-dT primed.
Average insert size 1.7 kb. Library enriched for full-length clones and constructed by Life Technologies.
Note: this is a NIH_MCC_Library."
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Search completed: November 6, 2002, 16:07:08 Job time: 269.086 secs
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                                                                                                                                                                                             253 CCAAGCCAAGCCAAATGGCCCCATCATCTCTCGCAAGAGCAGGAGAATACCTGGGGGCAG 312
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                                                                                                                                                                                                                                                                                         313 AGGCCATAG 321
                                                                                                                                                 183 CGTGGAGAG 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl7tl=PMO&t2=PMO-CTO642-
151200-001-g01&tz=2000-12-15&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 22
High quality sequence stop: 109.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="Organ: Colon; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196; 716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions. 81 t
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/clone_lib="CT0642"
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/db_xref="taxon:9606"
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Minimum DB
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       seq length: 0
seq length: 2000000000
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2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: .cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*
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Listing first 45 summaries
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10409
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80246
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US-08-869-477-1
US-09-009-119-1
US-09-009-119-1
PCT-US95-09098-1
US-08-72-240-3
US-08-72-2-177A-8
US-08-72-17-0-64-1
US-08-72-17-0-64-1
US-08-72-17-14-14
US-08-72-15-14
US-08-72-15-14
US-08-72-15-14
US-08-72-15-16-14
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Sequence 3, Appli
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Sequence 10, Appli
Sequence 11, Appli
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<u>, , , , , , , , , , , , , , , , , , , </u>	Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli	Sequence 3, Appli Sequence 3, Appli Sequence 3, Appli	Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 3, Appli	Sequence 3, Appli Sequence 3, Appli Sequence 5, Appli Sequence 3, Appli Sequence 133, App

## ALIGNMENTS

RESULT 1 US-08-142-439A-1

Sequence 1, Application US/08142439A Patent No. 5670360 GENERAL INFORMATION:

APPLICATION NUMBER: US/08/142,439A
FILING DATE: 24-NOV-93
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DK 398/92
FILING DATE: 25-NAR-92
PRIOR APPLICATION NUMBER: PCT/EP93/00697
FILING DATE: 23-NAR-93
ATTORNEY/AGENT INFORMATION:
NAME: Harrington, James J.
REGISTRATION NUMBER: 38,711
REGISTRATION NUMBER: 38,711
REFERENCE/DOCKET NUMBER: 3756.204-US
TELEPAN: 212 867 0123
TELEPAN: 212 867 0123 TELEFAX: 212 867 0298 INFORMATION FOR SEQ ID NO: TOPOLOGY: linear MOLECULE TYPE: CDN ZIP: 10174-6201 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy APPLICANT: Thorens, TITLE OF INVENTION: TITLE OF INVENTION: HYPOTHETICAL: NO ORIGINAL SOURCE: SEQUENCE CHARACTERISTICS:
LENGTH: 3066 base pairs
TYPE: nucleic acid CURRENT APPLICATION DATA: CORRESPONDENCE ADDRESS: NUMBER OF SEQUENCES: COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DC SOFTWARE: Patentin Release #1 CITY: New York
STATE: New York STREET: ORGANISM: STRANDEDNESS: single ADDRESSEE: NAME/KEY: CDS 405 Lexington Avenue, Suite 6400 U.S.A. IBM PC compatible SYSTEM: PC-DOS/MS-DOS linear No. US/08/142,439A 24-NOV-93 V: 530 Floppy disk 56703600 No. 5670360disk of No. 5670360th America, Inc. Receptor for the Glucagon-Like-Peptide-1 (GLP-1) 3756.204-US .0, Version #1.25

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US-08-142-439A-1
 Query Match
Best Local Similarity
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                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 1:
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                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/
FILING DATE: 23-MAR-93
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy
                                                                                                                   ORIGINAL
                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                           TELEPHONE: 212 867 0123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION:
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                                                                                                                             HYPOTHETICAL:
                                                                                                                                           MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 24-NOV-93
APPLICATION NUMBER: DK 398/92
FILING DATE: 25-MAR-92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                     TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                   NAME: Harrington, James J
REGISTRATION NUMBER: 38,7
                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Match 3.5%;
Local Similarity 92.4%;
                                                                                                   ORGANISM:
                                                                                                                                                           TOPOLOGY:
                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER:
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                                                                                                                                                                                                   LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New York
                                                                                                                 SOURCE:
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                                                                                                                                                                                                 3066 base pairs
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                                                                                                                                                                                                                                            212 867
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5 Lexington Avenue, Suite 6400
                                                                                                                                              CDNA
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 3.5%;
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                                                                                                                                                                                                                                                                                 38,711
ER: 3756.204-US
Score 58;
Pred. No.
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Pred. No. 4e-08;
DB 2;
4e-08;
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              Length 3066;
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; ORGANISM: Chlamydomonas reinhardtii US-09-371-507-1
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                    Query Match
Best Local :
                                                                                                                                              SEQ ID NO
                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1, Application US/09371507 Patent No. 6346656
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Patent No. 6160206
   Matches
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APPLICANT: BOYNTON, John E.
APPLICANT: GILLHAM, Nicholas W.
APPLICANT: HARRIS, Elizabeth H.
TITLE OF INVENTION: Porphyrin Accumulating-Type Herbicide Resistance Gene
FILE REFERENCE: Substitute sequence listing
CURRENT APPLICATION NUMBER: US/09/371,507
CURRENT FILING DATE: 1999-08-18
CURRENT FILING DATE: 1999-08-18
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Best Local Similarity 81.7%;
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APPLICANT: BOYNTON, John E.
APPLICANT: GILLHAM, Nicholas W.
APPLICANT: HARRIS, Elizabeth H.
APPLICANT: HARRIS, Elizabeth H.
APPLICANT: HARRIS, Elizabeth H.
TITLE OF INVENTION: Porphyrin Accumulating-Type Herbicide Resistance Gene
FILE REFERENCE: substitute sequence listing
CURRENT FILING DATE: 1998-01-20
RUMBER OF SEO, ID NOS: 1
ROMETUREN BEFORED WAS: 1
                                                                                                                                                             SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                  NUMBER OF SEQ ID NOS: 1
                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: 09/009,119 PRIOR FILING DATE: 1998-01-20
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TYPE: DNA
ORGANISM: Chlamydomonas reinhardtii
                                                                                                           TYPE: DNA
                                                                                                                          LENGTH: 3381
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 1 Similarity 67; Conserv
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                3.5%;
81.7%;
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Score 58; DB 4; Le
Pred. No. 4.2e-08;
0; Mismatches 15;
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Pred. No. 4.2e-08;
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                                   Length 3381;
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PCT-US95-09098-1/c
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             RESULT 6
US-08-772-440-33
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Sequence 33, Application US/08772440
                                                                                                                                                                                                                              Query Match
Best Local :
                                                                                                                                                                                                              Matches
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TELEX: 248345
INFORMATION FOR SEQ ID NO: 1:
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APPLICANT: Gillham, Nicholas W.
APPLICANT: Harris, Elizabeth H.
TITLE OF INVENTION: Porphyrin-Accumulating Type Herbicide
TITLE OF INVENTION: Resistance Gene
NUMBER OF SEQUENCES: 1
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 205-8000
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                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 3383 base pairs
TYPE: nucleic acid
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NAME: Murphy Jr., Gerald M.
REGISTRATION NUMBER: 28,977
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                           287 TTCCCTCCCTCCACTTCCTCCC 308
                                                                               1713 GTCCTGCAGCCCCGAACCCCGC 1692
                                                                                                                                                                                                                                                                                                                           ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                            HYPOTHETICAL: NO ANTI-SENSE: NO
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                                                                                                                                                                                                                                                                                     ORGANISM: CIL
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CITY: Falls Church
                                                                                                              287 TTCCCTCCCTCCACTTCCTCCC 308
                                                                                                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: PCT/US95/09098
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8110 Gatehouse Road, Suite 500 East
                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (703) 205-8050
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                                                                                                                                                                                                                                                                                                                                                                             DNA (genomic)
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 Mismatches

                                                                                                                                                                                                                                                 Length 3383;
                                                                                                                                                                                                                    Indels
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Patent No. 6046158 GENERAL INFORMATION:
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TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Ariizumi, Kiyoshi
APPLICANT: Takashima, Akira
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: UT
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
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FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: modified_base LOCATION: 3406..6470 OTHER INFORMATION: /mod_OTHER INFORMATION: /note
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TELEPHONE: 512/**-
TELEPHONE: 512/474-7577
TO ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: FILING DATE: CONCU
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: Houston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: nucleic acid
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            LOCATION: 3457..9998
OTHER INFORMATION: /mod_base= OTHER
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LOCATION:
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                                                                                               OTHER INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  modified_base
                                                                                                                                                                                                                                                                                                                                                                                            modified_base 3564..7896
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                                                                  modified_base
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           512/418-3000
                                                                                                                                                                                                                      3479..6422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CONCURRENTLY HEREWITH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    UNIQUE DENDRITIC CELL-ASSOCIATED C-TYPE LECTINS, DECTIN-1 AND DECTIN-2; COMPOSITIONS AND USES
                                                                                                                                                                                                                                                                                                                                                                                                                                                /note=
                                                                                                                                                                                                                                                                        /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "D = A or G or T"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US/08/772,440
                                                                                                                                                                                     /mod_base= OTHER
/note= "R = A or G"
                                                                                                                                                                                                                                                                          /mod_base= OTHER
/note= "N = A or C or G
                                                                                                                                                                                                                                                                                                                                                                                                                                                              /mod_base= OTHER
                                                                                                    /note=
                                                                                                                   /mod_base= OTHER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          32,165
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                                                                                                                                                                                                                                                                                                                                                             "M = A or C"
                                                                                                                                                                                                                                                                                                                                                                                                                                                "K - G or T"
                                                                                                      "S = C or G"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; OTHER INFORMATION: /mod_base= OTHER; OTHER INFORMATION: /note= "Y = C or T" US-08-772-440-33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 8, Application US/08222177A Patent No. 5582979
                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/341,562
FILING DATE: 21-APR-1989
ATTORNEY/ACENT INFORMATION:
NAME: Sara, Charles S.
REGISTRATION NUMBER: 30,492
REFERENCE/DOCKET NUMBER: 09865.601
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 108031-2100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION: APPLICANT: Weber,
POSITION IN GENOME:
                                 TISSUE TYPE: B
IMMEDIATE SOURCE:
                                                                                                    MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: LENGTH POLYMORPHISMS IN TITLE OF INVENTION: (dC-dA)n.(dG-dT)n SEQUENCES AND METHODS OF USING SAME NUMBER OF SEQUENCES: 460
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2825 GAGNNNNAAATTCAATANATAAAATTCTCTTTTGGCAGNTGAGTTCCTC 2872
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2765 ACACACACACACACAGTATGTCANNNAAACTCTGNAAGNTNTNATTAAAGATTCTCAT 2824
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             327 GAGATGACCATATTGACTGTAGAAATCACACCACCATAAAAGCCCCATC 374
                    CLONE:
                                                                   INDIVIDUAL ISOLATE
                                                                                         ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         267 ACACACACACATGTTTTCTTCCCTCCCTCCACTTCCTCCCATTCTCTGTGGTCCCAAA 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY:
                                                                                                                                                       STRANDEDNESS:
                                                                                                                                                                                                                                                                   TELEFAX: (608)
                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET:
                                                                                                                                                                                              LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Madison
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        53717-1914
                                                                                                                                                                           nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Wisconsin
                                                                                                                                                                                        200 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         E: DeWitt Ross & Stevens, S.C.
8000 Excelsior Drive, Suite 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            USA
                                                                                     Homo sapiens
                                                                                                                                          linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Weber, James L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 modified_base
3595..9999
                                                    Blood
                                                                                                                       DNA (genomic)
                                                                                                                                                          double
                                                                                                                                                                                                                                                                 831-2106
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56.0%;
                                                                   Caucasian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US/08/222,177A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 58; DB 3; Length 10409; Pred. No. 8.8e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    74; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
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US-08-920-422-17

: Sequence 17, Application US/08920422A

: Patent No. 6255473
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                                                                                                                                                                                                                            RESULT 8
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      GENERAL INFORMATION:

APPLICANT: Vitek, Michael P.

APPLICANT: Mitsuda, No. 6255473iaki

APPLICANT: Mitsuda, No. 6255473iaki

APPLICANT: Mitsuda, No. 6256473iaki

APPLICANT: MITSUDA, No. 6256473iaki

APPLICANT: MITSUDA, No. 6256473iaki

APPLICANTION: Presenilin-1 Gene Promoter

FILE REFERENCE: VITEKPRESENILIN

CURRENT APPLICATION NUMBER: US.08/920,422A
                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
CURRENT FILING DATE: 1997-08-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PUBLICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IDENTIFICATION METHOD: experimental OTHER INFORMATION: /evidence= EXPERIMENTAL OTHER INFORMATION: /standard_name= "Only or PUBLICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                       122 ACACACACACACACACTCACTCTCTCTCTCTCTG 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
                                                                                                                                                                                                                                                                                                                   283 TTTCTTCCCTCCCTCCACTTCCTCCATTCTCTGTG 318
                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   JOURNAL: NG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AUTHORS: Weber, James L.
AUTHORS: May, Paula E.
TITLE: Abundant Class of Human DNA Polymorphisms
TITLE: Which Can Be Typed Using the Polymerase Chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PAGES: 388-396
DATE: 1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VOLUME:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         JOURNAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AUTHORS: Weber, J. L. AUTHORS: May, P. E. TITLE: Dinucleotide repeat polymorphism at the D2S71 TITLE: locus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: /evidence= EXPERIMENTAL OTHER INFORMATION: /standard_name= "PCR primer" OTHER INFORMATION: /citation= ([1])
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PAGES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: misc_feature LOCATION: 1..200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LOCATION: complement (180..199) IDENTIFICATION METHOD: experime
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LOCATION: complement (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: /rpt_type= "tandem"
OTHER INFORMATION: /rpt_family= "(dC-dA)n.(dG-dT)n"
OTHER INFORMATION: /citation= ([2])
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LOCATION: 53..72
IDENTIFICATION METHOD:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Reaction
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nucleic Acids Res
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         3.5%;
75.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /evidence= EXPERIMENTAL
/standard_name= "PCR primer"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /standard_name= "Only one strand sequenced"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /citation= ([1])
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                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 57.6; DB Pred. No. 9e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 1; Length 200;
                                                                                                                                                                                                                                                                                                                                                                                                                                      24; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
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US-08-750-064-1
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                                            Query Match
              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1, Application US/08750064
Patent No. 6040142
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches 67; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQ ID NO 17
                                                                                                                                                                                                                                                                       TELEPHONE: (703) 816-4000
TELEFAX: (703) 816-4100
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           35891 ACACACACACACACACAAACA 35913
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS: 22
                                                                                                                  ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/750,064
FILING DATE: 29-JAN-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
ORGANISM: Mus musculus
                                                                                                                                ANTI-SENSE: NO
                                                                                                                                             HYPOTHETICAL:
                                                                                                                                                              MOLECULE TYPE:
                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 372 base pairs
TYPE: nucleotide
                                                                                                                                                                                                                                                                                                                   NAME: WILSON, MARY J. 2,955
REGISTRATION NUMBER: 32,955
REFERENCE/DOCKET NUMBER: 960
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION UNMBER: FR 94/06856
FILING DATE: 03-JUN-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: MELKI, JUDITH
APPLICANT: MUNNICH, ARNOLD
TITLE OF INVENTION: METHOD AND PROBES FOR DETECTING MARKERS
TITLE OF INVENTION: BOUND TO THE LOCUS OF CHILD SPINAL MUSCULAR ATROPHIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHYE P.C.
STREET: 1100 NORTH GLEBE ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 48974
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              257 ACACACACACACACACACACA 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A MATCH 75.3.4%; Score 57.2; DB 3; Length 372; Local Similarity 75.5%; Pred. No. 1.8e-08; Length 372; Nes 71; Conservative 0; Mismatches 23; Indels
                                                                                                                                                                                    TOPOLOGY:
                                                                                                                                                                                                 STRANDEDNESS:
                                                                                        ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: 1100 NOI
CITY: ARLINGTON
STATE: VIRGINIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22201-4714
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               U.S.A.
                                                                                                                                                                                    linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   E: Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                   ŏ
                                                                                                                                                                DNA (genomic)
                                                                                                                                                                                                    double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3.5%; Score 57.4; DB 4; Length 48974; 80.7%; Pred. No. 3.8e-07;
                                                                                                                                                                                                                                                                                                                                           960-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
   . 1.8e-08;
tches 23;
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     Indels
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Gaps
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; Sequence 4, Application US/09078294
; Patent No. 6265211
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                                      ; GENERAL INFORMATION:
                                                                                        US-09-078-294-4
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                                                                                                      RESULT 11
                                                                                                                                                                                                                                                                                                                                                       US-08-545-196B-14
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APPLICANT: Choo, Kong-Hong Andy APPLICANT: Du Sart, Desiree
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (703) 205-80 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: FARACI, C. J.
REGISTRATION UNMBER: 32,350
REFERENCE/DOCKET NUMBER: 2121
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: other nucleic acid DESCRIPTION: /desc = "SYNTHETIC DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: MELKI, JUDITH
APPLICANT: MUNICH, ARNOLD
TITLE OF INVENTION: SURVIVAL MOTOR NEURON (SMN) GENE: A GENE
TITLE OF INVENTION: FOR SPINAL MUSCULAR ATROPHY
NUMBER OF SEQUENCES: 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
                                                                                                                                                   145 CTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 178
                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS
                                                                                                                                                                                  284 TTCTTCCCTCCCTCCACTTCCTCCCATTCTCTGT 317
                                                                                                                                                                                                              145 CTCTCTCTCTCTCTCTCTCTCTCTCTCT 178
                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      284 TTCTTCCCTCCCTCCACTTCCTCCATTCTCTGT 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: FILING DATE: 19-OC
                                                                                                                                                                                                                                                                                                  Match 3.4%; Local Similarity 75.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: PO BOX 747
CITY: FALLS CHURCH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE:
                                                                                                                                                                                                                                                                                    71;
                                                                                                                                                                                                                                                                                                                                                                                                                                    nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  372 base pairs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        USA
                                                                                                                                                                                                                                                                                    Conservative
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RESULT 12
US-08-222-177A-14
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CURRENT FILING DATE: 1998-05-13
NUMBER OF SEQ ID NOS: 29
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Cancilla, Michael R.
TITLE OF INVENTION: A NOVEL NUCLEIC ACID MOLECULE
FILE REFERENCE: Davies Col
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION: APPLICANT: Weber,
                                                                                                                                                                                                                                       CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION UMBER: US 07/341,562
FILING DATE: 21-APR-1989
ATTORNEY/AGENT INFORMATION:
NAME: Sara, Charles S.
REGISTRATION NUMBER: 30,492
REGISTRATION NUMBER: 09865.601
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (608) 831-2100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  52119 ACACACACACACACACCCCCTATTCATTGCCAACAGTAATAGAGTTGCTTCTTTACT 52176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA ORGANISM: Nucleotide sequence of NC-contig
                                                                                                                                            INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 223 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 80246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: LENGTH POLYMORPHISMS IN TITLE OF INVENTION: (dC-dA)n.(dG-dT)n SEQUENCES AND METHODS OF USING SAME NUMBER OF SEQUENCES: 460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Flopy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS
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les 80; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE:
                                                                                                                                                                                                                     TELEFAX: (608) 831-2106
                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER:
TISSUE TYPE:
             ORGANISM: Homo sapiens INDIVIDUAL ISOLATE: Cau
                                                                                        TOPOLOGY:
                                                                                                          STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TTCCCTCCCTCCACTTCCTCCCATTCTCTGTGGTCCCAAAGAGATGACCATATTGACT 344
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                                                                                                                              nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          E: DeWitt Ross & Stevens, S.C.
8000 Excelsior Drive, Suite 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Weber, James L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                        linear
                                                                     DNA (genomic)
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                 Caucasian
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 38;
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                                                                                                             US-08-720-484A-1
                                                                                                                              RESULT 13
                                                                           Sequence 1, Application US/08720484A Patent No. 5990281
                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                           Matches
                                              GENERAL INFORMATION:
APPLICANT: DeSauv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PUBLICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE:
             APPLICANT: Rosenthal, Arnon APPLICANT: Stone, Donna
TITLE OF INVENTION:
                                                                                                                                                                              181 ACACATTCTTGCC 193
                                                                                                                                                                                                                                          JOURNAL:
VOLUME:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: OTHER INFORMATION:
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                                                                                                                                                                                                             279 ATGTTTTCTTCCC 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IDENTIFICATION METHOD: experimental OTHER INFORMATION: /evidence= EXPERIMENTAL OTHER INFORMATION: /standard_name= "Only or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IDENTIFICATION METHOD: experimental OTHER INFORMATION: /evidence= EXEERIMENTAL OTHER INFORMATION: /standard_name= "PCR primer" OTHER INFORMATION: /citation= ([1])
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AUTHORS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AUTHORS: May, P. E. TITLE: Dinucleotide repeat polymorphism at the TITLE: D18534 locus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LOCATION: complement (185..204)
IDENTIFICATION METHOD: experimental
                                                                                                                                                                                                                                                                                                                                                                                           PAGES: 388-
DATE: 1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PAGES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VOLUME:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     JOURNAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AUTHORS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: misc_feature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE:
                                                                                                                                                                                                                                                                                                                            Match 3.4%;
Local Similarity 86.3%;
                                                                                                                                                                                                                                                                                                             63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Reaction
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May, Paula E.
Abundant Class of Human DNA Polymorphisms
Which Can Be Typed Using the Polymerase Chain
                                                                                                                                                                                                                                                                                                                                                                                                           388-396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2201-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nucleic Acids Res.
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                                          DeSauvage, Frederic
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/rpt_family= "(dC-dA)n.(dG-dT)n"
/citation= ([2])
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /evidence= EXPERIMENTAL
/standard_name= "PCR primer"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /citation= ([1])
 Vertebrate Smoothened Proteins
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                                                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                                                                             Score 57; DB 1; Length 223
Pred. No. 1.5e-08;
0; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                                                                                    Gaps
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NUMBER OF SEQUENCES: 5

ADDRESSEE:

STATE:

South San Francisco

1 DNA Way

Genentech, Inc.

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RESULT 14
US-08-953-823A-1
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US-03-720-484A-1
                                                                                                                                                                                                                                                                                                                                                                             Sequence 1, Application US/08953823A Patent No. 6136958 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                    COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/953,823A
FILING DATE: 30-Sep-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS:
               PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                              TITLE OF INVENTION: VENUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
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MEDIUM TYPE: 3.5 inch, 1.44 mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Wilpatin (Genentech)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Svoboda, Craig G.
REGISTRATION NUMBER: 39,044
REFERENCE,DOCKET NUMBER: P10
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             276 CACATGTTTTCTTC 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION: NAME: Svoboda, Craig G.
                                                                                                                                                                                                                              STREET: 1 DNA Way
CITY: South San Francisco
APPLICATION NUMBER: 60/027070
                                  CLASSIFICATION:
                                                                                                                                                                                                  COUNTRY:
                                                                                                                                                                                                                     STATE:
                                                                                                                                                                                                                                                                ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
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STRANDEDNESS: Sing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/08/720,484A FILING DATE: 30-Sep-1996 CLASSIFICATION: 530
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                                                                                                                                                                                                                                                                                                                              DeSauvage, Frederic
Rosenthal, Arnon
Stone, Donna
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3.4%; Score 56.4; DB 2; Length 3854; 85.1%; Pred. No. 1.5e-07;
                                                                                                                                                                                                                                                                                                             Vertebrate Smoothened Proteins
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RESULT 15
US-08-232-463-14/c
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                           INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
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Best Local :
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INFORMATION FOR SEQ ID NO: 1:
                                                                                                          NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 300
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
                                                                                                                                                                                           FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                        CLASSIFICATION: 435
PRIOR APPLICATION UMBER: US/07/935,313
FILING DATE: EP 91 114 300.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKNER, F. G.
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA
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MEDIUM TYPE: Floppy disk
                                                                 TELLETAX: (/CT PX: 899149
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ATTORNEY/AGENT INFORMATION:
NAME: SVODOGA, CTaig G.
REGISTRATION NUMBER: 39,044
REFERENCE/DOCKET NUMBER: P1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
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LENGTH: 3854 base pairs
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                                                                                TELEPHONE: (/03/C-109)
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STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                        SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Alexandria
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                 nucleic acid
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1800 Diagonal Road,
                                                                                                                                                                                                                                                                                                                                                                                                                                                            USA
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; TOPOLOGY: linear
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Search completed: November 6, 2002, 14:19:56 Job time : 417.027 secs
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                                                                                                                                                                                                                                        625 GCTACTCTAACATTTTGTCTCTCACCTTCCACTTGGTTCTTCAATGGAAAGACTGGATAG 684
                                                                                                                                                                              505 GGGCTTGGTCAGCTAATGGAAATGATCTATGGTTTGACTTAAATGTGAAAGGAAAAAAA 564
                                                           745 CAAGCAGAGCCTTAGAGACAGAGAAGAGCCTGCTAGAGAYCATGAG 790
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Result
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Maximum Match 100%
Listing first 45 summaries
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Sequence:
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       1658.8
64.6
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DB seq length: 2000000000
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re greater than or equal to the score of the result being printed,
is derived by analysis of the total score distribution.

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1: /SIDS1/gcgdata/ge
2: /SIDS1/gcgdata/ge
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4: /SIDS1/gcgdata/ge
6: /SIDS1/gcgdata/ge
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8: /SIDS1/gcgdata/ge
9: /SIDS1/gcgdata/ge
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Match
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Copyright (c) 1993 - 2002 Compugen Ltd.
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/SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1986.DAT:*
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    2170
1199
245
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224
                      AAH43758
AAQ36051
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AAF98397
AAI88828
AAQ12760
ABL33197
AAK70103
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Human immune/haema
Human immune/haema
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Human secreted pro
3' portion of cDNA
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                                                                                                Human polynucleoti
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AASO4864 AASO6667 AAH40997 AAH23764 AAF85116 AAZ45596 AAZ52360 AAB121613 AAF21105 AAAF21105 AAAF21272 AAAF21272 AAAF21273 AAF21273 AAF21273 AAF21273 AAF21273 AAF21273 AAAF21273	AA190376 AAK81626 AAC91904 AAS16874 AAA39622 AAK66814 AAA39622 AAK66793 AAF21280 AAA35158 AAF21280 AAA35158 AAF2560 AAS46378 AAB132825 AAA35825 AAA5865750 AAF85750 AAF85750 AAF85750 AAF85750 AAF85750
Human chromosome 1 160kb fragment of 160kb fragment of Ruman chromosome 1 Nucleotide sequenc DNA sequence of th NSEQ gene-12 assoc Drosophila melanog Human low adenosin Human low adenosin Human adenosine re Human adenosine re Human low adenosine re Human polynucleoti Human polynucleoti Human foetal liver Probe #6724 for ge Human brain expres	Human polynucleoti Human immune/haema Murine A259 coding Murine A259 cDNA. Murine stomatin DN Human immune/haema Tumour suppressor Human low adenosine re Human low adenosine re Tumour suppressor Human adenosine re Tumour suppressor Human for affective Human immune syste Bipolar affective Human chromosome 1 Human chromosome 1

## ALIGNMENTS

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5' flanking region; 5' UTR; untranslated region; murine; glucagon-like peptide-2; GLP-2; receptor; regulator; intestinal epithelium; lateral hypothalamus; promoter; ds misc\_RNA misc\_RNA кеу WO200179290-A2 Mus musculus. 5' flanking and 5' UTR of GLP-2 receptor gene 30-JAN-2002 (first entry) AAH43758; AAH43758 standard; DNA; 2170 /\*tag= a
/note= "Punitive transcriptional start site"
1761..1763 /note= "Corresponds to translational start in rat/human GLP-2R gene" 1875..1877 Location/Qualifiers 1656 /\*tag= c /note= "Putative translational start site" ₿P

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25-OCT-2001.

12-APR-2001; 2001WO-IB00619

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Best Local Sim
Matches 1660;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    is useful for screening compounds to identify regulators of GLP-2 receptor expression. The DNA construct is also useful for delivering a gene product to tissues selected from intestinal epithelium and the lateral hypothalamus, by transfecting an organism, or a gametic or embryonic form of such an organism, with the construct. The DNA construct is also useful to identify cells capable of mediating expression from the chosen GLP-2R promoter, to identify regions of the GLP-2R promoter that are functional in a given cell type, and to screen for agents that modulate expression from the GLP-2R promoter. It can be used to map functional regions of the GLP-2R promoter, and for screening agents that modulate the function of GLP-2R promoter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This sequence represents the 5' flanking and 5' UTR of the murine glucagon-like peptide-2 (GLP-2) receptor gene. This sequence may be used in the DNA construct of the invention, such that it is linked for expression with a heterologous gene of interest. This construct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Fig 1; 70pp; English.
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01-FEB-2001; 2001US-265310P.
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                CCCTGTGAATGTTCAGAATTCACTGGGCTTGGTCAGCTAATGGAAATGATCTATGGTTTG
                                                                                                                         CATAAAAGCCCATCTGGGAGCCATTTCCAGACTGATCTTTTATCATTAAAGGTTTGAATT
                                                                                                                                                                                       TTCCTCCCATTCTCTGTGGTCCCAAAGAGATGACCATATTGACTGTAGAAATCACACCAC
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                                                                            CTTGCCACGTGTGGGTTTTAAGGTTTTTAGGGATTTTTATCTAGCGGCACTCACCTGCTT
                                                                                                          CATAAAAGCCCATCTGGGAGCCATTTCCAGACTGATCTTTTTTTCATTAAGGTTTGAATT
                                                                                                                                                                        TTCCTCCCATTCTCTGTGGTCCCAAAGAGATGACCATATTGACTGTAGAAATCACACCAC
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Similarity
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                                                                                                                                                                                                                                                                                                                     TGTCAGGTGGCCAGAGCATCACTGTGTTCAGAACACAACGGCCCACTCAGAACACGCGGGA 1140
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                                                                              TGAGGAAGTCCCAGGCAGCGTAGACGTCTTGGGGGTAGGTCTGGGAAAAATCTCCCCAAGA 1560
                                                                                                        GTGCGTAAGAATAGAATCCTCGGAATGGTAACCATGTCTTGCTTTTTCTTCTGGGCTTGC
                                                                                                                                                                          AGAAGCCTACCTGGCATGGGGGCCCATCCTCTCCAGCCATCCGAATCTCAATCTGGTCGT 1440
                                                                                                                                                                                                               CTGAGACAGGAAAACTCATCTTGTTACTATGGCATAGTAGTAACCACGGAGCTCTGAGAT 1320
                                                                                                                                                                                                                                                                                                                                                                          CAATTGAAAGGCACCAACCTCCGTGCTTCCTACCCGTTGTTTTGTTACCGTGTAAACGCA 1200
                                                                                                                                                                                                                                                                                                                                                                                                                               TGTCAGGTGGCCAGAGCATCACTGTGTTCAGAACACAACGGCCCACTCAGAACACGCGGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAQ36051;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (i.e. 50% formande, 5 x SCC). The promoter sequence from the human nov gene, localised to a 2.2kb pstI-HindII fragment and comprising the 283bp upstream of the start of exon 1 is specifically disclosed. The promoter sequence corresponds to sequence xxXIII which is given as three separate fragments in the specification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nucleotide sequences hybridising to regions of chicken useful as probes for detecting complementary sequences evaluate development and/or differentiation of tumours
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO9300430-A.
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                                                                                                                                                                                                                                                                                                                                       The human nov promoter contains several consensus sequences for different transcription factors such as NF1, API and Spl. It also comprises a sequence of 20 repeats of the TG motif ( a possible polymorphic marker). See also AAQ36050 and AAQ36052.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention includes nucleotide sequences which can hybridise to all or part of the chicken nov gene under stringent conditions (i.e. 50% formamide, 5 x SCC). The promoter sequence from the human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    07-JAN-1993
                                                                                                                                                                                                                                                                                                           Sequence 1199 BP; 269 A; 292 C; 248 G; 390 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Page 45-46; 67pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Martinerie C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25-JUN-1991;
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                                                                                                                                                                              1025 CAGGGGAAGGGAATCTAGAAAAAAATCGATATGTCAGGAGGTGGGGGAATGCTATTGG 966
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (CNRS ) CENT NAT RECH SCI.
                259
                                                                                                             965 CCAAATGGCAAAATTCTTTTGACTCTAATCCTTCTAGCTTCACTCAGTCTTAAACCCCCAA 906
                                                                                                                                             139 ATATTTGTACAAAACAGGTGCTTTCTCCCCCCACCATGCGACCCGGGAGCTCCACTGATAT 198
                                                                                                                                                                                                                                    3.9%;
Local Similarity 57.8%;
mes 115; Conserva+*...
                                                                                                                                                                                                              79 CAGGGGGAAGAAAATCAGGAAAAAAAAAATTTTTAGAAGCATTTCAAGAAGCAAGATGGA 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sapiens
ACACACACACACACACACA 277
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                                               (first entry)
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                                                                                                                                                                                                                                          Score 64.6; DB 14; Length 1199;
Pred. No. 2.6e-08;
0; Mismatches 84; Indels 0;
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AAV30918
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nucleic acid encoding secreted protein from human cells - useful, e.g. as immunomodulator, antitumour agent, promoters of tissue growth, haemostatic and thrombolytic agents etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Agostino MJ, Jacca
TA, Spaulding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAV30918 standard; DNA; 245 BP.
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25-OCT-1996;
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                                                                                                                                                                                                                                                                              Sequence 245 BP; 85 A; 69 C; 38 G; 45 T; 8 other;
                                                                                                                                                                                                                                                                                                                   proteins for analysis, characterisation, diagnostic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 16; Page 69; 114pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1998-261426/23.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (GEMY ) GENETICS INST INC.
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                          AAF98397;
                                                   AAF98397 standard; cDNA; 245 BP
                                                                                                                    133 CTTGCTTCCNTCCCCCAGTGCGTTCTGTGATCGCCAAG 170
                                                                                                                                             290
                                                                                                                                                                                                Local
                                                                                                                                                                       CCTCCCTCCACTTCCTCCCATTCTCTGTGGTCCCAAAG 327
                                                                                                                                                                                                                                       h 3.8%;
Similarity 77.6%;
                                                                                                                                                                                                                           Conservative
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aulding V,
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96US-0740274.
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                                                                                                                                                                                                                                       Score 63.4; DB 19;
Pred. No. 2.4e-08;
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07-JUN-2001

(first entry)

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RESULT 5
AAI8828/c
ID AAI888
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AAI888
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AO AAI888
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DT 06-NOV
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DT 06-Wman
LX
KW Human;
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                                                                                                                                                                                                                                                                                                                                                                              proteins AAB90667 - AAB90750. The cDNA clones are isolated from various tissue types, and may be used in the prevention, treatment and diagnosis of diseases associated with inappropriate protein expression. The polypeptides and nucleic acids may be used as nutrients or to modulate cytokine and cell proliferation/differentiation activity and may also be involved in modulation of the immune system. The cDNA sequences, proteins, their agonists and/or antagonists exhibit haematopoiesis regulating activity; tissue growth activity; activin/inhibin activity; chemotactic/chemokinetic activity; haemostatic and thrombolytic activity; receptor/ligand activity; anti-inflammatory activity; haematopoiesis activity, cadherin/tumour suppressor activity; and/or tumour inhibition activity. Included in the invention are probes represented in AAF98490 - AAF98572 which are specific for the cDNA clones
Human; cytokine; cell proliferation; cell differentiation; gene therapy;
                            Human polynucleotide SEQ ID NO 8888.
                                                       06-NOV-2001 (first entry)
                                                                                                              AAI88828 standard; cDNA; 353 BP
                                                                                                                                                                                                                                                                                                                                            Sequence 245 BP; 85 A; 69 C; 38 G; 45 T; 8 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human cDNA clones represented in AAF98374 - AAF98489 encode secreted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Page 405; 557pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Isolated nucleic acids encoding polypeptides, useful for modulating e.g. cytokine and cell proliferation/differentiation activity, the immune system and hematopoiesis regulating activity -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14-SEP-2000; 2000WO-US25135.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200119988-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; secreted protein; nutrient; cytokine modulator; proliferation; differentiation; immune system modulator; tissue growth; chemotactic; haemostatic; thrombolytic; anti-inflammatory; tumour inhibition; ss;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3' portion of cDNA encoding AS63_29 protein SEQ ID 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (GEMY ) GENETICS INST INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       haematopoiesis.
                                                                                                                                                                                                                                                           290 CCTCCCTCCACTTCCTCCCATTCTCTGTGGTCCCAAAG 327
                                                                                                                                                                                                                                  3.8%;
Local Similarity 77.6%;
es 76; Conservati...
                                                                                                                                                                           CTTGCTTCCNTCCCCCAGTGCGTTCTGTGATCGCCAAG 170
                                                                                                                                                                                                                                                                                                                                                                      the secreted proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                McCoy JM,
Treacy M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9908-0398829
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LaVallie ER,
Bowman MR,
                                                                                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                                                                                   Score 63.4; DB 22
Pred. No. 2.4e-08;
                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Spaulding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Collins-Racie LA,
Spaulding V, Agos
                                                                                                                                                                                                                                                                                                                DB 22;
                                                                                                                                                                                                                                                                                        22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Agostino MJ;
                                                                                                                                                                                                                                                                                                                Length 245;
                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Evans
                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                      0
В
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                                                                                                                                                                                                                                                                                     Вþ
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XX
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AAQ12760
                                                                                                                                                                                                                                                                                                                          RESULT 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to human polynucleotides (AAI79941-AAI93841) and the encoded proteins (AA000010-AA013910) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopolesis regulating activity, tissue growth factor activity, haematopolesis activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and
Mus musculus.
                                             T cell growth factor; AIDS; cytokine; T helper cell; ss
                                                                                                     P40 genomic DNA
                                                                                                                                                      17-OCT-1991 (first entry)
                                                                                                                                                                                                                 AAQ12760;
                                                                                                                                                                                                                                                                    AAQ12760 standard; DNA; 3809 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 353 BP; 65 A; 59 C; 108 G; 121 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; SEQ ID NO 8888; 1399pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Isolated nucleic acids and polypeptides, useful for preventing diagnosing and treating e.g. leukaemia, inflammation and immun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P-PSDB; AAO08897.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28-FEB-2000; 2000US-0515126
18-MAY-2000; 2000US-0577409
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                                                                                                                                                                                                                                                                                                                                                                                                            150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            inflammation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            286 CTTCCCTCCCTCCACTTCCTCCCATTCTC 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local
                                                                                                                                                                                                                                                                                                                                                                                                            ATTCCCTCCAGCCCGATTCCCCACATCTC 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity 80.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Drmanac RT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 61.8; DB 2:
Pred. No. 8.7e-08
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 353;
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0;

Location/Qualifiers

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Claim 1; Fig 15; 122pp; English
            Nucleic acid encoding for P40 T-cell growth factor - with AIDS or compromised immune systems, also allows prodn. of other cytokine(s).
                                                                                                                                                                                            misc_RNA
                                                                                                                                                                                                                        misc_RNA
                                                                                                                                                                                                                                                                             misc_RNA
                                                                                                                                                                                                                                                                                                                                                                                                                    exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                            exon
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                                                             Vansnick J,
                                                                          (RESE ) RES CORP TECHN INC
                                                                                         08-JAN-1990;
                                                                                                      08-JAN-1991;
                                                                                                                   25-JUL-1991
                                                                                                                               W09110738-A.
                                                                                                                                                                  misc_RNA
                                                                                                                                                                                                                                     polyA_signal
                                                                                                                                                                                                                                                  polyA_signal
                                                                                                                                                                                                                                                                                          sig_peptide
                                                                                                                                                                                                                                                                                                        TATA_signal
                                                                                                                                                                                                                                                                                                                            misc_signal
                                                                                                                                                                                                                                                                                                                                                       misc_signal
                                                                                                                                                                                                                                                                                                                                                                           misc_signal
                                                                                                                                                                                                                                                                                                                                                                                               misc_signal
                                         1991-238026/32.
DB; AAR13218.
                                                             Uyttenhove
                                                                                         90US-0462158
                                                                                                     91WO-US00145
                                                                                                                                                                                                                                              /_rawel= polyd-AdC_region
/note= "Z DNA; enhancer &
3582..3588'
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1361..1407
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589..594
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                                                                                                                                                                                                     /label= ATTTTA_motif
/note= " reduces sta
                                                                                                                                                                                                                       3523..3529
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                                                                                                                                                     /label=
                                                                                                                                                                       /label= ATTTTA_motif
/note= "_reduces stability of mRNA"
                                                                                                                                                                                                                 *tag=
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/label= C-rich
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                                                                                                                                                     ATTTTA_motif
                                                                                                                                             reduces stability of mRNA"
                                                                                                                                                                                                   reduces stability
                                                             Simpson
                                                                                                                                                                                                                                                                                                              binding
                    systems, also allows increased
                                                                                                                                                                                                                                                                                                              site"
                                                                                                                                                                                                                                                       activity"
                                                                                                                                                                                                   of mRNA"
                            for patients
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QΥ
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             a genomic library using a murine P40 cDNA clone as a probe. The sequence, or the cDNA sequence obtd. using the sequence, can be inserted into a vector for expression of P40 in a host organism. The protein is useful for stimulating the proliferation of certain subsets of T helper cells e.g. in AIDS patients or immune
                                                                                    Claim 1; SEQ ID NO 1170; 32pp + Sequence Listing; German.
                                                                                                                           Nucleic acid comprising fragment of chemically modified for diagnosis and treatment of diseases associated with
                                                                                                                                                                 WPI;
                                                                                                                                                                                                                                              30-JUN-2000;
01-SEP-2000;
                                                                                                                                                                                                                                                                                  02-JUL-2001;
                                                                                                                                                                                                                                                                                                                                     WO200200928-A2
                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                   acute myelold leukaemia; Alzheimer's disease; AIDS; epilepsy; neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease;
                                                                                                                                                                                                                                                                                                                                                                                                                 neuroprotective; anti-HIV; anticonvulsant; ophthalmological; antirheumatic; antiarthritic; antidabetic; antipsoriatic; antiinflammatory; cancer; eye disease; arteriosclerosis; anaemia; acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; immune system disease; cytosine methylation; antiasthmatic;
antiarteriosclerotic; antianaemic; cytostatic; nootropic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human immune
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See also AAQ12759 and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The
                                                                                                              cytosine methylation
                                                                                                                                                                                                                     (EPIG-)
                                                                                                                                                                                                                                                                                                            03-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                        gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26-MAR-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1412 CTTTCTCTGGCATCTTCCTACTCTTTCCCCTTCCCAGT 1449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               280 TGTTTTCTTCCCTCCCTCCACTTCCTCCCATTCTCTGT 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sequence was obtd. from a clone,
                                                                                                                                                                 2002-130909/17.
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                                                                                                                                                                                                                     EPIGENOMICS AG
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                                                                                                                                                                                          Piepenbrock C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                            2000DE-1032529
2000DE-1043826
                                                                                                                                                                                                                                                                                    2001WO-EP07537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           system associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
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76.5%;
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                                                                                                                                                                                           Berlin
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Pred. No. 4.9e-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gene SEQ ID NO: 1170
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
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                                                                                                                          gene, useful
abnormal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3809;
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The present invention provides a number of human immune system associated genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis,

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RESULT 8
AAK70103
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Best Local S
Matches 66
31 - JAN - 2000
24 - FEB - 2000
24 - FEB - 2000
10 - MAR - 2000
11 - MAR - 2000
20 - JUN - 2000
20 - JUN - 2000
20 - JUN - 2000
21 - JUL - 2000
21 - AUG - 2000
22 - AUG - 2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel diseases. The present sequence is a gene of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 6183 BP; 1584 A; 230 C; 1532 G; 2837 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        17-JAN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                09-AUG-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200157182-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cytostatic; gene therapy; vaccine; metastasis; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human immune/haematopoietic antigen genomic sequence SEQ ID NO:24915
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      06-NOV-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAK70103;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ch 3.7%;
l Similarity 88.0%;
66; Conservative
2000US-0179065.
2000US-0184664.
2000US-0186364.
2000US-0188974.
2000US-0198123.
2000US-020515.
2000US-0214886.
2000US-0214886.
2000US-0214886.
2000US-0214886.
2000US-0214886.
2000US-0214896.
2000US-021489.
2000US-0217496.
2000US-0217496.
2000US-0218290.
2000US-0218290.
2000US-0228513.
2000US-0228575.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 60.6; DB 24;
Pred. No. 9.6e-07;
0; Mismatches 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 6183;
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  23 AUG-2000
30 AUG-2000
31 SEP-2000
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14 SEP-2000
15 SEP-2000
16 SEP-2000
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18 NOV-2000
19 SEP-2000
19 SEP-2000
19 SEP-2000
10 SEP
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2000US-0228924.
2000US-0229287.
2000US-0229343.
2000US-0229344.
2000US-0229345.
2000US-022959
2000US-022959
2000US-0230438
2000US-0231244
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2000US-0232397
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2000US-0249207
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                                                                                                                                                                                                                                                 ARK54951 to ARK64702 encode the human immune/haematopoietic antigen (I) amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic c activity, and can be used in gene therapy and vaccine production. (I) CC proteins and polynucleotides may be used in the prevention, diagnosis and c treatment of diseases associated with inappropriate (I) expression. For CC example, they may be used to treat disorders associated with decreased cc expression by rectifying mutations or deletions in a patient's genome CC that affect the activity of (I) by expressing inactive proteins or to c supplement the patients own production of (I). Additionally, (I) CC polynucleotides may be used to produce the secreted (I), by inserting CC the nucleic acids into a host cell and culturing the cell to express the CC protein. (I) proteins and polynucleotides may be used to prevent, CC diagnose and treat immune/haematopoietic-related diseases, especially cancers and cancer metastases of haematopoietic-derived cells. AAK64703
                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                          Matches
23698 ATCCCTCACTTCTCTTAAGCCAA 23720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17-NOV-2000
17-NOV-2000
17-NOV-2000
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01-DEC-2000
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08-DEC-2000
08-DEC-2000
                                                                                                                                                                              Sequence 23885 BP; 6416 A; 5634 C; 5563 G; 6272 T; 0 other;
                                                                                                                                                                                                         to AAK87694 represent human immune/haematopoietic antigen genomic sequences from the present invention. AAK54942 to AAK54950 and AAM82169 represent sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nucleic acids encoding useful for preventing,
                             287 TTCCCTCCCTCCACTTCCTCCCA 309
                                                      Disclosure; SEQ ID NO 24915;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              metastasis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2001-483426/52.
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17-NOV-2000;
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                                                                                                                        Conservative
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2000US-0256719.
2000US-0251479.
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2000US-0249245
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2000US-0254097
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2000US-0251030
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2000US-0249265
                                                                                                                3.7%; Score 60.6; DB 22; Length 23885; 83.1%; Pred. No. 2e-06; tive 0; Mismatches 14; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     human immune/hematopoietic antigen polypeptides, diagnosing and/or treating cancers and
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Gaps

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RESULT 9
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22 - AUG - 2000)
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14-AUG-2000;
14-AUG-2000;
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07-JUL-2000;
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07-JUN-2000;
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cytostatic; gene therapy; vaccine; metastasis; ds.
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26-JUL-2000;
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2000US-0215135.
2000US-0216647.
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2000US-0228924.
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2000US-0225270
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2000US-0218290
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2000US-0217487
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04-CCT-2000

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12-SEP-2000;
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14-SEP-2000;
21-SEP-2000;
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29-SEP-2000;
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25-SEP-2000;
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2000US-0231968.
2000US-0232397.
2000US-0232398.
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2000US-0235836.
2000US-0236327.
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2000US-0234997.
2000US-0234998.
2000US-0235484.
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2000US-0246526.
2000US-0246528.
2000US-0246532.
2000US-0246610.
2000US-0246611.
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2000US-0249207.
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2000US-0249211.
2000US-0249213.
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2000US-0241809
2000US-0241826
2000US-0244617
2000US-0246474
2000US-0246474
2000US-0246476
2000US-0246476
2000US-0246476
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2000US-0249244.
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06-NOV-2001 (first entry)

Human polynucleotide SEQ ID NO 10436.

Human; cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorders; arthritis; inflammation; ss.

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AAI90376 standard; cDNA; 415

ВР

23698 ATCCCTCACTTCTCTTAAGCCAA 23720

287 TTCCCTCCCTCCACTTCCTCCCA 309

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В
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                                                                                                                                                                                        CC amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic contivity, and can be used in gene therapy and vaccine production. (I) corrections and polynucleotides may be used in the prevention, diagnosis and cax they may be used to treat discorders associated with inappropriate (I) expression. For comple, they may be used to treat discorders associated with decreased comple; they may be used to treat discorders associated with decreased comple; they may be used to treat discorders associated with decreased comple; they may be used to treat discorders associated with decreased comple; the patients own production or deletions in a patient's genome complement the patients own production of (I). Additionally, (I) complement the patients own production of (I). Additionally, (I) concerned and creat immune/haematopoietic decided to prevent, complement to a host cell and culturing the cell to express the content of the present immune/haematopoietic antigen genomic concerned and cancer metastases of haematopoietic antigen genomic concerned and concerned invention. AAK54942 to AAK87493 and AAM82169 concerned and the present invention. AAK54942 to AAK87493 and AAM82169 concerned and the present invention. AAK54942 to AAK87493 and AAM82169 concerned and the present invention. AAK54942 to AAK87493 and AAM82169 concerned and the present invention.
                                                                       Matches
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01-DEC-2000

01-DEC-2000

05-DEC-2000

05-DEC-2000

06-DEC-2000

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; SEQ ID NO 27985; 3071pp + Sequence Listing; English.
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                                                                                                                                           Sequence 23885 BP; 6416 A; 5634 C; 5563 G; 6272 T; 0 other;
                                                                                                                                                                              represent sequences used in the exemplification of the present invention
                                 Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CA,
                                                                       69;
                                                                                        Similarity
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                                                                     Conservative
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2000US-0251990.
2000US-0254097.
2001US-0259678.
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2000US-0256719
2000US-0251479
2000US-0251868
2000US-0251868
2000US-0251869
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2000US-0251030
                                                                                        3.7%;
83.1%;
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                                                                         Mismatches
                                                                       Score 60.6; DB 22;
Pred. No. 2e-06;
0; Mismatches 14;
                                                                           Indels
                                                                                                         Length 23885;
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RESULT 11
AAK81626
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Best Local 9
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                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to human polynucleotides (AAI79941-AAI93841) and the encoded proteins (AAO00010-AAO13910) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, hammatopoiesis regulating activity tissue growth factor activity, immunomodulatory activity and activin/inhibin activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and
      09-AUG-2001
                         W0200157182-A2
                                                              cytostatic; gene therapy; vaccine; metastasis; ds.
                                                                         Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
                                                                                                                       07-NOV-2001
                                              Homo sapiens.
                                                                                              Human immune/haematopoietic antigen genomic sequence SEQ ID NO:36438
                                                                                                                                            AAK81626;
                                                                                                                                                                AAK81626 standard; DNA; 8095
                                                                                                                                                                                                                                                                                                                                             Sequence 415 BP; 130 A; 109 C; 63 G; 112 T; 1 other;
                                                                                                                                                                                                                                                                                                                                                                          Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; SEQ ID NO 10436; 1399pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Isolated nucleic acids and polypeptides, useful for preventing diagnosing and treating e.g. leukaemia, inflammation and immune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                P-PSDB;
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18-MAY-2000; 2000US-0577409.
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                                                                                                                                                                                                                                                                                                                                                                    ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                      ACACACACACACACACACACACACACACACATGTTTTCTT 288
                                                                                                                                                                                                                                                                                                       76;
                                                                                                                                                                                                                                                                                                                   Similarity
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                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                3.6%;
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24-FEB-2000;
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2000US-0232081.
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2000US-0220963
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2000US-0217487
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2000US-0205515
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20-OCT - 2000;
20-OCT
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WP,I; 2001-483426/52
                                                      Rosen CA,
                                                                                                             HUMAN GENOME SCI INC
                                                      Barash SC,
                                                                                                                                                             2000US-0249297

2000US-0249300

2000US-0249300

2000US-0250160

2000US-0251030

2000US-0251030

2000US-0251988

2000US-0251479

2000US-0251856

2000US-0251868

2000US-0251869

2000US-0251869

2000US-0251869

2000US-0251869

2000US-0251869

2000US-0251989

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2000US-0251989

2000US-0251989
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2000US-0249214

2000US-0249215

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2000US-0249218

2000US-0249218

2000US-0249244

2000US-0249245

2000US-0249265
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2000US-0246611.
2000US-0246613.
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2000US-0249208.
2000US-0249209.
2000US-0249210.
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2000US-0246478
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2000US-0246476.
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2000US-0240960.
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2000US-0246527.
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2000US-0246609
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                                                      Ruben SM;
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Matches Query Match Best Local (

1 Similarity 81.4 70; Conservative

0;

Score 60.4; DB 22; Pred. No. 1.3e-06; 0; Mismatches 16;

Length 8095; Indels

0

Gaps

0;

3.6%;

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expression by rectifying mutations or deletions in a patient's genome that affect the activity of (I) by expressing inactive proteins or to supplement the patients own production of (I). Additionally, (I) polynucleotides may be used to produce the secreted (I), by inserting the nucleic acids into a host cell and culturing the cell to express the protein. (I) proteins and polynucleotides may be used to prevent, diagnose and treat immune/haematopoietic-related diseases, especially cancers and cancer metastases of haematopoietic-derived cells. AAK64703 to AAK87694 represent human immune/haematopoietic-derived cells acceptable sequences from the present invention. AAK84942 to AAK54950 and AAM82169 represent sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                 AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I) amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic activity, and can be used in gene therapy and vaccine production. (I) proteins and polynucleotides may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate (I) expression. For example, they may be used to treat disorders associated with decreased
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 8095 BP; 2662 A; 1135 C; 1557 G; 2741 T; 0 other;
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AAC91904
                                                                                                                                                                                                                                                                                                                                 7247
                                                                                                                                                                         Murine; A259; integrin alpha subunit; fibrosis; liver disease; lung; kidney; cancer; osteoporosis; acute myeloid leukaemia; HIV infection; rheumatoid arthritis; ss.
                                                                                                                                                                                                                          19-MAR-2001 (first entry)
                                                                                                                                                                                                                                                                                                   7307 CACACACACACACACACACACACA 7332
                                                                                        mat_peptide
                                                                                                        sig_peptide
                                                                                                                                                          Mus sp.
                                                                                                                                                                                                         Murine A259 coding sequence
                                                                                                                                                                                                                                           AAC91904;
                                                                                                                                                                                                                                                           AAC91904 standard;
                                                                WO200073339-A1.
                                                                                                                                                                                                                                                                                                                   254 CACACACACACACACACACACACACA 279
                                                                                                                                                                                                                                                                                                                                                 /*tag= a
/product=
28..93
/*tag= b
94..3591
/*tag= c
                                                                                                                                         Location/Qualifiers
                                                                                                                                  28..3594
                                                                                                                                                                                                                                                           4858 BP
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28-MAY-1999; 99US-0322790 27-APR-2000; 2000US-0561263

99US-0322**7**90

15-MAY-2000; 2000WO-US13262

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Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present sequence is the coding sequence for murine integrin alpha subunit, A259. A259 is homologous with the alphal and alphal0 integrin subunits and is overexpressed in fibrosis. A259 is implicated in regulation of proliferation, differentiation and/or function of many different cell types. Inhibitors of A259 activity are useful for the treatment of liver disease, particularly fibrosis, and also fibrosis in other organs (specifically lung and kidney). In addition, A259 can be used for treatment and prevention of cancer, osteoporosis, acute myeloid of treatment and prevention of cancer, osteoporosis, acute myeloid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; Fig 5; 164pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nucleic acid encoding alpha-integrin subunits, useful for treatment and diagnosis of fibrosis, e.g. of the liver \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4398
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                                                                                                                                                                                                                    Mouse; A259; integrin alpha subunit; integrin alpha 10; secreted protein; liver disease; fibrosis; lung; kidney; bone associated disorder; blood; cartilage associated disorder; haematopoietic disorder; bone marrow; ss; immune related disease; apoptotic disorder; neuronal tissue disease; neurodegenerative disease; gene therapy; cancer; cytostatic; osteopathic; nephrotropic; immunomodulator; anti-inflammatory; neuroprotective; antiarthritic; antianemic; antiallergic; antiasthmatic; dermatological;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 4858 BP; 1184 A; 1397 C; 1296 G; 981 T; 0 other;
                                                                                                                                                                                                                                                                                                                                           Murine A259
                                                                                                                                                                                                                                                                                                                                                                         14-FEB-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                    AAS16874 standard; cDNA; 4858
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       mat_peptide
                                                                    sig_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 leukaemia, HIV infection, and rheumatoid arthritis.
                                                                                                                                                                             Mus musculus.
                                                                                                                                                                                                           antidiabetic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    299 A 299
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                                                                                                                                                                                                                                                                                                                                              CDNA.
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                                                                                                                                                                                                           anticonvulsant; antiparkinsonian.
                                        /*tag=
94..35
                                                                      /note- "This 28..93
                                                                                                                /*tag=
                                                                                                                                 28..3594
            /product= "Mature murine A259"
                                                                                                    /product= "Mouse A259"
                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3.6%;
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Pred. No. 1.1e-06;
                                                                                    coding sequence is specifically claimed"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 22;
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AAA39622
                                                                                                                                                                                                                             RESULT 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             which encode secreted proteins with homology to integrin alpha subunits, specifically to integrin alpha 10. The A259 polypeptide and nucleic acid are useful for treating liver disease or fibrosis, particularly kidney fibrosis or lung fibrosis. The A259 polypeptide and nucleic acid are also useful for diagnosing, preventing or treating cartilage and bone associated disorders (such as bone cancer, achondroplasia, myeloma,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        fibrous dysplasia, scoliosis, osteoarthritis, osteosarcoma and scute mysplasia, scoliosis, osteoarthritis, osteosarcoma and scute mysplasia, scoliosis, osteoarthritis, osteosarcoma and scute mysplasia, bone marrow, blood and haematopoietic disorders (such as erelated diseases (such as HIV, viral infections, cancers, T cell autoimmune disorders e.g. AIDS, and allergic inflammatory disorders e.g. asthma and psoriasis), apoptotic disorders (such as systemic lupus erythematosus and insulin-dependent diabetes mellitus), diseases of the neuronal tissues (such as epilepsy and muscular dystrophy) and neurodegenerative diseases (such as Parkinson's disease and Huntington's periodegenerative diseases (such as Parkinson's disease).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New A259 nucleic acids and polypeptides, which comprise integrin alpha subunit, useful for diagnosing, preventing or treating e.g. liver disease, kidney or lung fibrosis, cancers, blood disorders or immune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-2001.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             related diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P-PSDB; AAU10552
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27-APR-2001; 2001WO-US13516
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 4858 BP; 1184 A; 1397 C; 1296 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (MILL-) MILLENNIUM PHARM INC
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                                                                                                              01-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                  4458
                                  Stomatin; murine; treatment; pain; analgesic; anesthetic;
                                                                        Murine stomatin DNA
                                                                                                                                                   AAA39622;
                                                                                                                                                                                         AAA39622 standard;
                                                                                                                                                                                                                                                                                                                                                                                                        239
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                                                                                                                                                                                                                                                                                                                                                                83;
                                                                                                                                                                                                                                                                                                                            299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This sequence represents cDNA encoding the murine A259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                              (first entry)
                                                                                                                                                                                           DNA; 1787
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    to human and murine A259 nucleic acid molecules
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 60.2;
Pred. No. 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1.1e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      981 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 4858;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                          allodynia;
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Gaps

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4457 298

diagnostic;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This invention describes a novel protein (I) of the stomatin family which can be used in the treatment of pain. (I) is involved in transduction of mechanical stimuli to a receptor potential, particularly in perception of pain and contact, so when the function of (I) is reduced, so will be sensitivity to pain. (I) and other members of the stomatin family, are used as target proteins for treatment of pain, and especially: (1) for the development of analgesics and anesthetics, e.g for treating allodynia; (2) for constructing genes and vectors, particularly for pharmaceutical development; (3) for developing diagnostic kits for predicting an individual's response to different analgesics/anesthetics or disposition to side effects, and (4) for determining disposition to disease. This sequence encodes the murine stomatin protein described in the method of the invention.
           WQ200157182-A2
                                                                     Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
cytostatic; gene therapy; vaccine; metastasis; ds.
                                                                                                              Human immune/haematopoietic antigen genomic sequence SEQ ID NO:21626.
                                                                                                                                                06-NOV-2001 (first entry)
                                                                                                                                                                                                                                                                                           1113 AACAACAACAACAAAAACCA 1132
                                                                                                                                                                                                                                                                                                                                                  AAK66814 standard; DNA; 5176 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New stomatin family protein, useful as target for developing e.g. analgesics and anesthetics, is involved in pain and contact perception {\bf r}
                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2000-330220/29.
P-PSDB; AAY87912.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
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                                                               21-SEP-2000;
25-SEP-2000;
25-SEP-2000;
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08-SEP-2000;
08-SEP-2000;
08-SEP-2000;
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08-SEP-2000;
08-SEP-2000;
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17-MAR-2000;
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14-JUL-2000;
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19-MAY-2000;
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                                             2000US-0234998.
2000US-0235484.
              2000US-0235834.
2000US-0235836.
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2000US-0234997.
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2000US-0233065.
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2000US-0232398.
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2000US-0232400.
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WPI; 2001-483426/52

Rosen CA,

Barash SC,

Ruben SM;

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Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis -
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Disclosure; SEQ ID NO 21626; 3071pp + Sequence Listing; English.

amino acid sequences given in AAM82170 to AAM81921. (I) have cytostatic cartivity, and can be used in gene therapy and vaccine production. (I) cyroteins and polynucleotides may be used in the prevention, diagnosis and carament of diseases associated with inappropriate (I) expression. For cerample, they may be used to treat disorders associated with decreased cexpression by rectifying mutations or deletions in a patient's genome that affect the activity of (I) by expressing inactive proteins or to complement the patients own production of (I). Additionally, (I) complement the patients own production of (I). Additionally, (I) complement coids into a host cell and culturing the cell to express the protein. (I) proteins and polynucleotides may be used to prevent, complement coids into a host cell and culturing the cell to express the complement of the proteins and polynucleotides may be used to prevent, complement and cancer metastases of haematopoietic cantiden genomic concers and cancer metastases of haematopoietic antigen genomic concers from the present invention. AAK54942 to AAK54950 and AAM82169 crepresent sequences used in the exemplification of the present invention. AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I) amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic

Sequence 5176 BP; 1472 A; 1210 C; 1170 G; 1324 T; 0 other;

Q В δõ Query Match Best Local : Matches 879 ACCTCTCTATCCCTTCTCT 287 TICCCTCCCTCCACTICCT 305 Local 67; 3.6%; Similarity 84.8%; Conservative Score 59.8; DB 22 Pred. No. 1.5e-06; Mismatches DB 22; 12; Indels Length 5176; 0; Gaps 0

Search completed: November Job time: 510.209 secs 6 2002, 14:16:40

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## ALIGNMENTS

BASE COUNT	FEATURES source	TITLE JOURNAL	AUTHORS	REFERENCE	SOURCE ORGANISM	KEYWORDS	ACCESSION VERSION	LOCUS DEFINITION	RESULT 1 AX354807
/organism="synthetic construct" /db_xref="taxon:32630" /note="Recombinant DNA expression construct" 574 a 500 c 551 g 540 t 5 others	Location/Qualifiers 12170	Glp-2 receptor gene promoter and uses thereof Patent: WO 0179290-A 1 25-OCT-2001; 1149336 OWTARIO INC. (CA)	Drucker, D.J. and Lovshin, J.A.	artificial sequence. 1 (sites)	synthetic construct. synthetic construct		AX354807 AX354807.1 GI:18619538	AX354807 2170 bp DNA linear PAT 06-FEB-2002 Sequence 1 from Patent W00179290.	

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Submitted (17-JAN-2001) Department of Medicine, University of
Toronto, 101 College Street CCRW3-845, Toronto, ON M5G2C4, Canada
                                                                                                                                                                           Lovshin, J.A., Estail, J., Yusta, B., Brown, T.J. and Drucker, D.J. Glucagon-like Peptide (GLP)-2 Action in the Murine Central Nervous System Is Enhanced by Elimination of GLP-1 Receptor Signaling J. Biol. Chem. 276 (24), 21489-21499 (2001)
                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 3130)
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                                                            TTTTAGGAGGGCAGGCGGGGATGAGAAACTTGGAGATTCGGTAGATCGCTGTAGAGCA
                                                                                                                         TGAGGAAGTCCCAGGCAGCGTAGACGTCTTGGGGGTAGGTCTGGGAAAAATCTCCCCAAGA
                                                                                                                                                  GTGCGTAAGAATAGAATCCTCGGAATGGTAACCATGTCTTGCTTTTTCTTGGGCTTGC
                                                                                                                                                                                                                                                                TGTCAGGTGGCCAGAGCATCACTGTGTTCAGAACACAACGGCCCACTCAGAACACGCGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GAACAAACACCCTGGCCTCTTTGAACCCCACTATTTCTCAGCCCTCAGATGAAGAAGTAA
ACTCAGACAGTCGGCGGCCTGAAGAGGACTTGTGCAAAACA
                        ACTCAGACAGTCGGCGGCCTGAAGAGGACTTGTGCAAACA 1660
                                                TTTTAGGAGGGGCAGGCGGGGATGAGAAACTTGGAGATTCGGTAGATCGCTGTAGAGCA
                                                                                                  TGAGGAAGTCCCAGGCAGCGTAGACGTCTTGGGGGTAGGTCTGGGAAAAATCTCCCAAGA
                                                                                                                                                                                                   AGAAGCCTACCTGGCATGGGGGCCCATCCTCTCCAGCCATCCGAATCTCAATCTGGTCGT
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VERSION
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                                                                                                                                                                                                      DEFINITION
                 AUTHORS
TITLE
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                                                                                                                                                                  207160 bp DNA linear :
Mus musculus chromosome 11 clone RP23-409J21 map 11,
SEQUENCE, 21 unordered pieces.
Mus musculus chromosome Unpublished 2 (bases 1 to 207160)
                   Mahimatta, ....
1 (bases 1 to 207160)
Birren,B., Linton,L., Nusbaum,C. and Lander,E.
... mirronlus chromosome 11, clone RP23-409J21
                                                                                                           Mus musculus
                                                                            Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                          AC016464.3 GI:7137319
HTG; HTGS_PHASE1; HTGS_DRAFT
                                                                                                                             house mouse.
                                                                            Chordata;
Rodentia;
                                                                            Craniata; Vert
Sciurognathi;
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Vertebrata; Euteleostomi;

HTG 01-MAR-2000

Muridae;

Murinae; Mus

Length

length length length

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COMMENT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Tirrell, A., Vassiliev, H., Vo, A., Wheeler, J., Wu, X., Wyman, D., Ye, W.J., Zimmer, A. and Zody, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Baldwin, J., Barna, N., Beckerly, R., Boguslavkiy, L., Boukhgalter, B., Brown, A., Castle, A., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Domino, M., Donelan, L., Doyle, M., Ferreira, P., Fitzhugh, W., Forrest, C., Funke, R., Gage, D., Ferreira, P., Fitzhugh, W., Forrest, C., Funke, R., Gage, D., Ferreira, P., Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L., Galagan, J., Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L., Galagan, J., Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L., Galagan, J., Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L., Galagan, J., Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L., Galagan, J., Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L., Galagan, J., Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L., Galagan, J., Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L., Galagan, J., Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L., Galagan, J., Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L., Galagan, J., Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L., Galagan, J., Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L., Galagan, J., Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L., Galagan, J., Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L., Galagan, J., Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, G., Gardyna, G., Gar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (30-NOV-1999) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Mar 1, 2000 this sequence version replaced gi:6970326.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Howland, J.C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., Leu, C., Locke, K., Macdonald, P., Marquis, N., McBurk, A., McKernan, K., McLaughlin, J., Meldrim, J., Morrow, J., Naylor, J., Norman, C. H., O'Connor, T., O'Donnell, P., Peterson, K., Pollara, V., Riley, R., Roy, A., Santos, R., Severy, P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Birren,B., Linton,L., Nusbaum,C., Lander,E., Allen,N., Anderson,M., Baldwin,J., Barna,N., Beckerly,R., Boguslavkiy,L., Boukhgalter,B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NOTE: This is a 'working draft' sequence. It currently consists of 21 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            as soon as in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequencing vector: M13; M77815; 100% of reads Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.960731 Consensus quality: 196848 bases at least 040 Consensus quality: 202204 bases at least 030 Consensus quality: 202204 bases at least 030 Consensus quality: 20206 bases at least 030 Insert size: 210000; agarose-fp Insert size: 205160; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Center clone name: 409_J_21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Quality coverage: 4.8 in Q20 bases; agarose-fp Quality coverage: 4.9 in Q20 bases; sum-of-contigs
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25539 25638:
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642 1859: contig of 1218 bp in length
                                                                                                             40233:
        55451:
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12095: gap of 6357 t
12095: gap of 100 t
40133: con-
                         233: gap of 100 bp
48264: contig of 8031 bp
364: gap of 100 bp
55351: contig of 6987 bp

    Genome Center

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18479: contig of 4235
579: gap of 100 by
25538: contig of 6959
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149263 149362: g
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                                                                              /note="assembly_fragment"
177678. .207160
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149363. .177577
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63946: gap of 100 bp
75456: contig of 11510 bp in length
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149362: contig of 18868 bp
149362: gap of 100
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Similarity 99.0%, Score 160.2; DB 2; Length 207180; Similarity 99.0%, Score 160.2; DB 2; Length 207180; SI; Conservative 3; Mismatches 6; Indels 8; daps 7777 (Conservative 3; Mismatches 6; Indels 8; daps 7774 (Conservative 4; Mismatches 6; Mismatc
Similarity
96.58; SCOTE 1501.2) DB 2; Length 207180; CONSERVATIVE 3; MISMATCHES 6; Indels 8; Gaps ACCGCARTITICACACAGAGGGAAGAAAACAGGGAGGAGGAGGAGGAGGAG
96.5%; Score 1601.2; DB 2; Length 207160; 99.0%; Pred. No. 0; 91.11111111111111111111111111111111111
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S 6; Indels 8; Gaps  CCACGGGTAGCAGGTCATGAAGCT 60
S 6; Indels 8; Gaps  CCACGGGTAGCAGGTCATGAAGCT 60
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                                                                                                                                                                                                                                                                                                     Submitted (08-JAN-2002) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CBLO 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk on Jan 11, 2002 this sequence version replaced gi:18072579.
                                                                                                                                                                                                                         "" DNA linear HTG 10-JAN-2002 Mus musculus chromosome 11 clone RP23-338M9, *** SEQUENCING IN PROGRESS ***, in unordered pieces.
AL646097
            Center project name: bM338M9
                                                                                                                                                                                                    AL646097.5 GI:18135259
HTG; HTGS_PHASE1; HTGS_DRAFT.
                             Contact: humquery@sanger.ac.uk
                                                             Center code:
                                                                                                                                Direct Submission
                                                                                                                                         Mclay,K
                                                                                                                                                             Eukaryota; Metazoa;
Mammalia; Eutheria;
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Assembly program: XGAP4; version 4.5
                                                 Web site:
                                                                     Center: Wellcome Trust Sanger Institute
                                                                                                                                                                                          house mouse.
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           Summary Statistics
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953 AGAAGTAATGGTACCTTGGAGGATACTGATGGGTTCAAGTGAACTAGGGCAGAGGGTGGA 1012
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                                                                                                                                                                      355 CACCACCATAAAAGCCCCATCTGGGAGCCATTTCCAGACTGATCTTTTTATCATTAAGGTT 414
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TAAACGCAACTCAACTCTCGGCACTGAACAGGCTTTTGCTGCAGACCTGGGGTCTGGAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CACGTGGACAATTGAAAGGCACCAACCTCCGTGCTTCCTACCCGTTGTTTTGTTACCGTG 132643
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CACGCGGACAATTGAAAGGCACCAACCTCCGTGCTTCCTACCCGTTGTTTTGTTACCGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAAATATCTGTCAGGTGGCCAGAGCATCACTGTGTTCAGAACACAACGGCCCACTCAGAA 132703
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAAATATCTGTCAGGTGGCCAGAGCATCACTGTGTTCAGAACACAACGGCCCACTCAGAA 1132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TCCCAAGATTTTAGGAGGGGCAGGCGGGGGATGAGAAACTTGGAGATTCGGTAGATCGCT 1612
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TGTTGTCTCTGAGACAGGAAAACTCATCTTGTTACTATGGCATAGTAACCACGGAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 6 from Patent WO0179290.
                                                                                                                                                                                                          Glp-2 receptor gene promoter and uses thereof patent: WO 0179290-A 6 25-OCT-2001; 1149336 ONTARIO INC. (CA)
                                                                                                                                                                                                                                                                                   Drucker, D.J. and Lovshin, J.A.
                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                              AX354812.1
                                                                                                                                                                                                                                                                                                      (sites)
                                                                                                               /organism="Mus sp."
/db_xref="taxon:10095"
/protein_id="CAD22992.1"
/db_xref="GI:18619544"
                                           /codon_start=
                                                                 /note="unnamed protein product"
                                                                                                                                                                                 ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                 GI:18619543
                                                                                              .>466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA
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KEYWORDS
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                                                                                                                                                  COMMENT
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TITLE
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                                                                                                                                                                                           JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1534 GGTAGGTCTGGGAAAAATCTCCCCAAGATTTTAGGAGGGGCAGGCGGGGGATGAGAAACTT 1593
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1474 ATGTCTTGCTTTTCTTCTGGGCTTGCTGAGGAAGTCCCAGGCAGCGTAGACGTCTTGGG 1533
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1654 GCAAACA 1660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GCAAACA 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             186;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N., Anderson,S., Baldwin,J., Barna,N., Bastien,Y., Beda,F., Boguslavkiy,L., Boukhgalter,B., Brown,A., Burkett,G., Campoplano,A., Castle,A., Choepel,Y., Colangelo,M., Collins,S., Collymore,A., Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S., Collymore,A., Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACO26591 198271 bp DNA linear Homo sapiens chromosome 17 clone RP11-655D3 map 17, IN PROGRESS ***, 4 ordered pieces.
                                                                                          submitted (22-MAR-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA on Aug 26, 2001 this sequence version replaced gi:14547870. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 (bases 1 to 198271)
Birren,B., Linton,L., Nusbaum,C. and Lander,E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HTG; HTGS_PHASE2; HTGS_FULLTOP; HTGS_ACTIVEFIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AC026591.9 GI:15291083
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens chromosome 17, clone RP11-655D3
                                                                         http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mammalia; Eutheria;
                                                                                                                                                                                                                      Direct Submission
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                             Center: Whitehead Institute/ MIT Center for Genome
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132 c 155 g 104 t 2 ot
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                                                       Genome Center
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
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27-AUG-2001 SEQUENCING

Research

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Db 145200 ACAAAACCAAAAACGAAGTGAAAACATGTTCTTCTTGCCTCTTGCTGACTCACTGTTCCA 145141
                                                                                                                                                                                                               Db 145298 CTGCTTTTCCCCAACTGTTCAGAATTCATTCAGTTGAAAAGTTACCCAGGATGAGTTCCTA 145239
                                                                                                                                                                                                                                                                                                                  Db 145358 TAAAATCTTGTCACATGGAGTTTTTAAGATTTTTAGGGATGTCTATTAAGAAAAGCATGG 145299
                                                                                                                                                                                                                                                                                                                                                                                                                        Db 145418 CACCACTCTGAGTCCATTTCTAGGGTCTTTGTTCTAGTTGAGCTTTTCATTGTTAAGGTC 145359
                                                                                                              Db 145238 TGTTTGACTTGAAGAGGAAGGAAAAAATA-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Db 145533 AGTTGCAGCCACATTCAATGAC-----CAAAGTCCATCCCTTGGGTACTTTCTCCCTCTG 145479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Db 145589 ACCATTTTCCAGC----ATGCAACTTGGAAGATGATCTTTAATGAGCACTCACAGAACGG 145534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Db 145649 AAAAGTTGCAAGAGATGAGATGGAATATTCTTGCAAAGCAGGTATTTTCTTTAAAGACAG 145590
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              145478 GGTCACTCCTGCTCTCTGCCATCCCAGAGAGATGACCACGTCAATTCCAGAGGTGA 145419
                                                 595 GGGAAGGGAAAACTGCCTTTTATGCCTATTGCTACTCTAACATTTTGTCTCTCACCTTCC 654
                                                                                                                                       475 CTGCTTCCCTGTGAATGTTCAGAATTCACTGGGCTTGGTCAGCTAATGGAAATGATCTAT 534
                                                                                                                                                                                                                                                                                                                                                   415 TGAATTCTTGCCACGTGTGGGTTTTTAAGGTTTTTTAGGGATTTTTATCTAGCGGCACTCAC 474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  115 AAGCATTTCAAGAAGCAAGATGGAATATTTGTACAAAACAGGTGCTTTCTCCCCCCACCAT 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                            355 CACCACCATAAAAGCCCATCTGGGAGCCATTTCCAGACCTGATCTTTTTATCATTAAGGTT 414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                295 CTCCACTTCCTCCCATTCTCTGTGGTCCCCAAAGAGATGACCATATTGACTGTAGAAATCA 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            175 GCGACCCGGGAGCTCCACTGATATGGACAGAATAGCTTTACAGCTACATTCAAAACACAC 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

1 133566: contig of 133566 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NOTE: This is a 'working draft' sequence. It currently consists of 4 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   52858 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            153567 153666: gap of
153667 158888: contic
158889 158988: gap of
158989 189474: conti
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone="RP11-655D3"
/clone_lib="RPCI-11 Human Male BAC"
/clone_lib="RPCI-11 Human Male BAC"
/ 45543 c 46237 g 53270 t 363 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /chromosome="17"
/map="17"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
/db_xref="taxon:9606"
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	Qy 1655 CAAACA 1660
1654	QY 1599 TTCGGTAGATCGCTGTAGAGCAACTCAGACAGTCGGCGGCCTGAAGAGGACTTGTG
1598	Qy 1554 CCCAAGATTTTAGGAGGGCAGGCGGGGGATGAGAAACTTGGAGA
r 1553 r 1441	Qy 1494 GGCTTGCTGAGGAAGTCCCAGGCAGCGTAGACGTCTTGGGGGTAGGTCTGGGGAAAAATCT 
3 1493 3 1442	Qy 1448AGAATAGAATCCTCGGAATGGTAACCATGTCTTGCTTTTCTTCTG
- 1447 C 14431	Qy 1409 CTCTCCAGCCATCCGAATCTCAATCTGGTCGTGTGCGTA
C 1408	Qy 1351 TGATGCTTTAGAAAGAAATCGTGGCTTAAAAGAAGCCTACCTGGCATGGGGGCCCATC
T 1350     14443	Qy 1299 AGTAACCACGGAGCTCTGAGATAGCCCTGAGCTGGTGCCGTTTAGAAAAGTT
T 1298     14449	Qy 1239 CTGGGGTCTGGAGGTTTGTCTCTGAGACAGGAAAACTCATCTTGTTACTATGGCATAGT
C 1238 G 14455	179
T 1178	QY 1119 CGGCCCACTCAGAACACGCGGACAATTGAAAGGCACCAACCTCCGTGCTTGCT
A 1118 C 1446	QY 1059 CCATGAATACCATAAAAATATCTGTCAGGTGGCCAGAGCATCACTGTGTTCAGAACACAA
G 1058	QY 999 GGGCAGAGGGTGGAAGGTTTTGTAACCATAAACTGAAGTGGGGTGTTAGTTA
A 998   A 1447	QY 940 AGCCCTCAGATGAAGAAGTAATGGTA-CCTTGGAGGATACTGATGGGTTCAAGTGAACTA
C 939	QY 880 TTTTGCTTGCTGTGCAGCCTTGAACAAACACCCTGGCCTCTTTGAACCACCACTATTTCTC
T 879	QY 828 CTAACCAGGTAGCTGTGGTCACGTGACTCGGCTGGAAGSCCTGGCTTTGTCT
C 827	75 T
3C 774 3G 1450	QY 715 GTGTGTGTGTGTGGGGGGGGGGGGGGAGCAAGCAGAGACCTTAGAGAGACAGAGAAGAGCCC
3A 714   3G 1450	Qy 655 ACTTGGTTCTTCAATGGAAAGACTGGATAGAAAGCTGGGAGCCAGCC

runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence. as soon as it is available and the accession number will

be preserved

75255 75354: gap of 100 bp 75355 76881: contig of 1527 bp in length 76882 76981: gap of 100 bp 76982 78538: contig of 1557 bp in length

75254: contig of 75254 bp in length

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Db 144074 CAAACA 144069
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REFERENCE
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1 (bases 1 to 210719)
Birren, B., Linton, L., Nusbaum, C. and Lander, E.
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O'Connor,T., O'Donnell,P., O'Neil,D., Oliver,J., Peterson,K.,
Phunkhang,P., Pierre,N., Pollara,V., Raymond,C., Retta,R.,
Rieback,M., Riley,R., Rise,C., Rogov,P., Roman,J., Rosetti,M.,
Rieback,M., Schauer,S., Schupback,R., Seaman,S., Severy,P.,
Roy,A., Santos,R., Schauer,S., Schupback,R., Seaman,S., Severy,P.,
Sougnez,C., Spencer,B., Stange-Thompson,S., Stojanovic,N.,
Strauss,N., Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J.,
Travers,M., Travis,N., Trigilio,J., Vassiliev,H., Viel,R., Vo,A.,
Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G., Zainoun,J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE, 12 unordered pieces. AC087646
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Research, 320 Charles Street, Cambridge, MA 02141, USA On May 31, 2001 this sequence version replaced gi:13493095. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html
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Homo sapiens chromosome 17 clone RP11-773021 map 17, WORKING DRAFT
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                       * NOTE: This is a 'working draft' sequence. It currently consists of 12 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (15-JAN-2001) Whitehead Institute/MIT Center for Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Direct Submission
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                                                                                                                                                                    Sequencing vector: plasmid; n/a; 100% of reads Sequencing vector: plasmid; n/a; 100% of reads Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.960731 Consensus quality: 205962 bases at least Q40 Consensus quality: 208431 bases at least Q30 Consensus quality: 209403 bases at least Q20 Insert size: 205000; agarose-fp Theory is a consensus quality: 209109 bases; agarose-fp Quality coverage: 8.4 in Q20 bases; sum-of-contigs Quality coverage: 8.2 in Q20 bases; sum-of-contigs
arbitrary. Gaps between the contigs are represented as
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: sequence_submissions@genome.wi.mit.edu
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Butheria; Primates; Catarrhini; Hominidae; Homo.
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sum-of-contigs
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FEATURES

194086

ocation/Qualifiers

.210719

100 bp

105001 105100: gap of 100 bp in length 105101 121101: contig of 16001 bp in length 121102 121201: gap of 100 bp in length 121202 154071: contig of 32870 bp in length 154072 154171: gap of 100 bp 154172 193985: contig of 39814 bp in length

701: gap of 100 bp 105000: contig of 15299 bp in length 109: gap of 100 bp 89601: contig of 3192 bp in length

100 bp 82098: contig of 2052 bp in length 198: gap of 100 bp 86309: contig of 4111 bp in length

79946:

gap of

p of 100 bp contig of 1308 bp in length

86410 86310 86409: 82099 82198: 79947 80046: 78539 78638:

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                            115 AAGCATTTCAAGAAGCAAGATGGAATATTTGTACAAAACAGGTGCTTTCTCCCCCCACCAT 174
                                                                         Local Similarity
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89702, 105000
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194086. .210719
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                                                           2; Mismatches 696;
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                                                                                         Length 210719;
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1238 72713	9 GTTTTGTTACCGTGTAAACGCAACTCAACTCTCGGCACTGAACAGGCTTTTGCTGCAGAC 	117 7276	P 6
1178 72768	19 CGGCCCACTCAGAACACGCGGACAATTGAAAGGCACCCAACCTCCGTGCTTCCTACCCGTT	111 7282	p 4
1118 72828	39 CCATGAATACCATAAAAATATCTGTCAGGTGGCCAGAGCATCACTGTGTTCAGAACACAA	105 7288	P 49
1058 72888	9 GGGCAGAGGG 	و ق	B 3
998 72944	10 AGCCCTCAGATGAAGAAGTAATGGTA-CCTTGGAGGATACTGATGGGTTCAAGTGAACTA 	94 7300	P 6
939 73004	O TTTTGCTTGCTGTGC	88 7306	D Qy
879 73064	0 - i		B 4
827 73124	5 TGCTAGAGAYCATGAGCTTYCTTTGAGACCCCTAGTGCTAACAGGAA 3 GAGGCATGGCGATGAGCCTGCTAAGAACTCACCGGAGAGGGCAGGGC		B 64
774 73184	S GTGTGTGTGTGTGTGGGGGGGGGGGGGGGCAGCAAGCAGAGCCTTAGAGACAG ACGCTGGGAGCTGGCCTGGGAGAGAGGTGGAGTAAGAAGTTCCAAGCAG		B 5
714 73240	5 ACTTGGTTCTTCAATGGAA 		β Q
654 73300	95 GGGAAGGGAAACTGCCTTTTATGCCTATTGCTACTCTAACATTTTGTCTCACCTTCC		P 04
594 73360	5 GGTTTGACTTAAATGTGA		p Q
534 73398	5 CTGCTTCC		g Q
474 73458	15 TGAATTCTTGCCACGTGTGGGTTTTAAGGTTTTTAGGGATTTTATCTAGCGGCACTCAC	735	D
414 73518	55 CACCACCATAAA            77 CACCACTCTGAG	735	B 6
354 73578	95 CTCCACTTCCTCCCATTCTCTGTGGTCCCAAAGAGATGACCATATTGACTGTAGAAATCA 	736	d da
73638	35 ACACACACACACACACACACACACACACACACACACAC	736	D Q
73693	75 GCGACCCGGGAGCTCCACTGATATGGACAGAATAGCTTTACAGCTACATTCAAAACACACAC	1 737	D Qy

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REFERENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 72412 AGCCTGTCAAGGAAGTCCCCAGAAAGCACAGCTGACTT-AGGGAAGGTCTGGGAAAAATCT 72354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                72592 TAATGCCTTAGAAAGAAATACCCTGCCTCAAAAAGACACCTGCCTCTAAACTGGCTCGAG 72533
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1655 CAAACA 1660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1494 GGCTTGCTGAGGAAGTCCCAGGCAGCGTAGACGTCTTGGGGGTAGGTCTGGGAAAAATCT 1553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1554 CCCAAGATTTTAGGAGGGGCAGGCGGGGGATGA------GAAACTTGGAGA 1598
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1239 CTGGGGTCTGGAGGTGTTGTCTCTGAGACAGGAAAACTCATCTTGTTACTATGGCATAGT 1298
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TTCGTGCATTGAGCAGAACCTTCAGGGTGGAGCCCGCCTGACCGCCTTGTTCTTCTCCTC 72413
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAACAGGACCCAGAGGAGATTTTGCCTTTGTGGTTAGCCTCAGCCCAGCCTGGACAAGCT 72593
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----AGAATAGAATCCTCGGAATGGTAACC----ATGTCTTGCTTTTCTTCTG 1493
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Web site:http://genome.wustl.edu/gsc/index.shtml
                                                                                                                                                                                        Center: Washington University Genome Sequencing Center Center code: WUGSC
                                                                                                                                                                                                                                                                                                           Direct Submission
Submitted (16-MAY-2000) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St.
                                                                                                                                                                                                                                                                           MO 63108, USA
On Dec 11, 20
                                                                                                                                                                                                                                                                                                                                                                              2 (bases 1 to 213359)
Waterston, R.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 213359)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AC069006 213359 bp DNA linear HTG 11-DEC-2000 Homo sapiens chromosome RPCI-11 clone RP11-773021, WORKING DRAFT SEQUENCE, 16 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                      The sequence of Homo sapiens clone Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Waterston, R.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HTG; HTGS_PHASE1; HTGS_DRAFT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AC069006.4 GI:11612641
                                                                                                                                                                                                                                                                     2000 this sequence version replaced gi:9280811
                                                                                                                                                                                                                                   ---- Genome Center ----
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Insert size: 211859; sum-of-contigs
Ouality coverage: 5.34 in Q20 bases;
Quality coverage: 5.44 in Q20 bases;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Consensus quality: 203603 bases at least Q40 Consensus quality: 206822 bases at least Q30 Consensus quality: 208592 bases at least Q20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NOTE: This is a 'working draft' sequence. It currently consists of 16 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence
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            /note="assembly_name:Contig25"
40515. .53087
                                                                 vector_side:right"
24763. .32389
                                                                                             clone_end:T7
                                                                                                                                                                                                   /note="assembly_name:Contig19"
4722. .7894
                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
/db_xref="taxon:9606"
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/note="assembly_name:Contig26"
                                                   /note="assembly_name:Contig24"
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                                                                                                                                                           /note="assembly_name:Contig21"
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contig of 25957 bp in
gap of unknown length
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contig of 3121 bp
gap of unknown ler
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contig of 13760 bp in
gap of unknown length
contig of 16011 bp in
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of 12573 bp
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CTAACCAGGTAGCTGTGGTCACGTGACTCGGCTGGAAGSCCTGGC-----TTTGTCT 879
                                                                                         GAGGCATGGCGATGAGCCTGCTAAGAACTCACCGGAGAGGGCAGGGGCAGGACAGGGCAC 84363
                                                                                                                                                                                                        ACGCTGGGAGCTGGCCTGGGAGAGGTGGAGTAAGAAGTTCC----AAGCAGAGCCTTTGG 84423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GGGAAGGGAAAACTGCCTTTTATGCCTATTGCTACTCTAACATTTTGTCTCTCACCTTCC 654
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CTGCTTTTCCCAACTGTTCAGAATTCATTCAGTTGAAAAGTTACCCAGGATGAGTTCCTA 84637
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TAAAATCTTGTCACATGGAGTTTTTAAGATTTTTAGGGATGTCTATTAAGAAAAGCATGG 84697
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TGAATTCTTGCCACGTGTGGGTTTTAAGGTTTTTAGGGATTTTTATCTAGCGGCACTCAC 474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CACCACTCTGAGTCCATTTCTAGGGTCTTTGTTCTAGTTGAGCTTTTCATTGTTAAGGTC 84757
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACCATTTTCCAGC----ATGCAACTTGGAAGATGATCTTTAATGAGCACTCACAGAACGG 84932
                                                                                                                                                                                                                                                              GTGTGTGTGTGTGGGGGGGGGGGGGCAGCAGCAGAGCCTTAGAGACAGAGAAGAGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                      ACAAAAACCAAAAACGAAGTGAAAACATGTTCTTCTTGCCTCTTGCTGACTCACTGTTCCA 84539
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171277. .213359
/note="assembly_name:Contig33"
47447 c 48599 g 56470 t
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/note="assembly_name:Contig27"
64777. .78536
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/note="assembly_name:Contig31
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117563. .143519
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Pred. No. 2.9e-19;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ----ACACAAAA 84599
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                                                                                                                                                                                                                                                                                                                DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                 AC100859
                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT
                                                 ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               83472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             84302 GTTTACTTGCTGTGTGGCTTTGGGCAAGCCATCCAACCTCTCTGAGCCTCAATGTTTCTC 84243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   84362 CCTCCCAAGTACCTGTGCTCAAGCAACTCTGGTCAGAAGACCTGCCTATCCGGTTCTGCT 84303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GCAAACA 1660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTCGGTAGATCGCTGTAGAGCCAACTCAGACAGTC----GGCGGCCTGAAGAGGGACTTGT 1653
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CAGCCTGTCAAGGAAGTCCCAGAAAGCACAGCTGACTT-AGGGAAGGTCTGGGAAAAATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GGGCTTGCTGAGGAAGTCCCAGGCAGCGTAGACGTCTTGGGGGTAGGTCTGGGAAAAATC 1552
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CTGGTCGTGTGCGTAAGAATAGAATCCTCGGAATGGTAACCATGTCTTGCTTTTTCTTCT 1492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GCCCATCCTCCAGCCATCCGAATCTC-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CTGGGGTCTGGAGGTGTTGTCTCTGAGACAGGAAAACTCATCTTGTTACTATGGCATAGT 1298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GTTTTGCTATTGTGTAGGCATAACCTA-----CGCCGCTGATTGGGTTTTTGCTTCATGG 83952
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CCATGAATACCATAAAAATATCTGTCAGGTGGCCAGAGCATCACTGTGTTCAGAACACAA 1118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AGCTGTCAAATGGAGAATTCATCGTATCCTCATGGGGTTATTGTCAGGATGTGCGAAATA 84183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AGCCCTCAGATGAAGAAGTAATGGTA-CCTTGGAGGATACTGATGGGTTCAAGTGAACTA 998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GCAAACA 83466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TCCCTGCTTTTGGGGGGGCAGGGGCGGGGGATGAGCCCAGGGCCGAGAAGGAACTCTGAAG 83533
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TAATGCCTTAGAAAGAAATACCCTGCCTCAAAAAGACACCTGCCTCTAAACTGGCTCGAG 83772
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TGATGCTTTAGAAAGAAATCGTGGCTTAAAAGAAG-----CCTACCTGGCATGGGG 1401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAACAGGACCCAGAGGAGATTTTGCCTTTGTGGTTAGCCTCAGCCCAGCCTGGACAAGCT 83832
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AGTAACCACGGAGCTCTGAGATAGCCCT-----GAGCTGGTGCCGTTTAGAAAAGTT 1350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CCTGGGCTGGGAGCTGTTCTCCTGAGCTGAGCAACCACCTCTCCTGCAGTCTCTGCAT 83892
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GTTTTGTTACCGTGTAAACGCAACTCAACTCTCGGCACTGAACAGGCTTTTGCTGCAGAC 1238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACATGTGCTTAGAACAAGTGGGCATTCAAGATGAGTGAATGTTGCACTTTTCAACACACT 84007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CGGCCCACTCAGAACACGCGGACAATTGAAAGGCACCAACCTCCGTGCTTCCTACCCGTT 1178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GCTGGTTAGTAAGTGATGTATCATCAATTCCATAAAAGGGTCTGTCAGGTGGGCTGAGCC 84067
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GGATGGTGGGTTAAAAGACGT----TGTCAATGTGAGTTGTGGGGGACAGCCTACTCCTGT 84127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TTTTGCTTGCTGTGCAGCCTTGAACAACACCCTGGCCTCTTTGAACCCCCACTATTTCTC 939
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TCCCAAGATTTTAGGAGGGGCAGGCGGGGGATGA------GAAACTTGGAG 1597
                                                                                                                                                                                                                           SEQUENCE SAMPLING AC100859
                                                                                                                                                                                                                                                                                                                                                    AC100859
                                                 Homo sapiens
                                                                                                                                                                              AC100859.1 GI:17048229
                                                                                                                                                                                                                                                                                                            Homo sapiens chromosome
                                                                                                                                 HTGS_PHASEO.
                                                                                                                                                                                                                                                                                                            clone RP11-615H7 map 15,
                                                                                                                                                                                                                                                                                                                                                    DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----AAT 1432
                                                                                                                                                                                                                                                                                                                                               linear
                                                                                                                                                                                                                                                                                                            HTG 22-NOV-2001
LOW-PASS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE
AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hagos, B., Heaford, A., Horton, L., Hulme, W., Illev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., LaRocque, K., Lamazares, R., Landers, T., Lehoczky, J., Levine, R., Liu, G., MacLean, C., Macdonald, P., Major, J., Marquis, N., Matthews, C., McCarthy, M., McEwan, P., McKernan, K., McPheeters, R., Meldrim, J., Mcneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P., Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schupback, R., Seaman, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Yiel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Anderson, S., Barna, N., Bastien, V., Boguslavkiy, L., Boukhgalter, B., Brown, A., Camarata, J., Campopiano, A., Chang, J., Chazaro, B., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cook, A., Cooke, P., DeArellano, K., Dewar, K., Dlaz, J.S., Dodge, S., Faro, S., Ferreira, P., Fitchugh, W., Gage, D., Galagan, J., Gardyna, S., Gord, S., Gord, S., Gord, S., Gord, S., Gord, S., Gord, S., Horton, L., Hulme, W., Iliev, I., Johnson, R., Hagos, B., Heaford, A., Horton, L., Hulme, W., Iliev, I., Johnson, R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, p. (1996–1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (22-NOV-2001) Whitehead Institute/MIT Center Research, 320 Charles Street, Cambridge, MA 02141, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Birren, B., Linton, L., Nusbaum, C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished
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Birren,B., Linton,L., Nusbaum,C. and Lander,E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sequencing reads that have not been assembled into contigs. Runs of N are used to separate the reads and the order in which they appears completely arbitrary. Low-pass sequence sampling is useful for identifying clones that may be gene-rich and allows overlap relationships among clones to be deduced.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  However, it should not be assumed that this clone will be sequenced to completion. In the event that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the record
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NOTE: This record contains 61 individual
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (bases 1 to 49665)
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                                                                                                                                                                                                                      5509
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4667: contig of 697 bp in
668 4767: gap of 100 bp
768 5508: contig of 741 bp in 1
09 5608: gap of 100 bp
09 6347: contig of 739 bp in 1
18 6447: gap of 100 bp
7 7296: gap of 100 bp
7 7296: gap of 100 hp
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                                                                                                                                                                                                                                                                                                                                                                 2300: contig of 676 bp in 14

2400: gap of 100 bp

3073: contig of 673 bp in 1e

173: gap of 100 bp

3870: contig of 697 bp in 1er

170: gap of 100 bp

170: gap of 100 bp
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    Genome Center

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Stojanovic, N.
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11292 11391:

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14588 14687; gap of 100 bp 11 length 15513 15512; gap of 100 bp 16180 16279; contig of 667 bp in length 15513 16179; contig of 667 bp in length 16280 16504; contig of 667 bp in length 16280 17064; gap of 100 bp 17065 17765; contig of 685 bp in length 17785 17885; contig of 721 bp in length 17786 17885; gap of 100 bp 18618 18717; gap of 100 bp 18618 18717; gap of 1726 bp in length 1874 1543; gap of 100 bp 19544 19543; contig of 732 bp in length 1618 18717; gap of 100 bp 19544 19543; contig of 736 bp in length 1618 20279; contig of 736 bp in length 1618 20379; gap of 100 bp 100 
                                                                                                                                                                                                                                                     24329
25249
25348: gap of
25349
26080: contig of 732 bp in length
26081
26181
26082: contig of 669 bp in length
26550
26949: gap of
26950
27692: contig of 743 bp in length
27693
27792: gap of
27793
28519: contig of 727 bp in length
28520
28619: gap of
28620
29317: contig of 792 bp in length
29318
29417: gap of
2010 bp
30120
3019: contig of 702 bp in length
30220
30926: contig of 707 bp in length
3027
31026: gap of
31027: contig of 707 bp in length
3178
31828
31271: contig of 707 bp in length
3158
31827: gap of
31028
33944: contig of 737 bp in length
32658
33944: contig of 737 bp in length
3395
33495
3423: contig of 730 bp in length
3423: contig of 730 bp in length
3423: contig of 730 bp in length
34224 34323: gap of 100 bp

34324 35057: contig of 734 bp in length

35058 35157: gap of 100 bp

35158 35866: contig of 709 bp in length

35867 35966: gap of 100 bp

36867 36786: gap of 100 bp in length

36687 36786: gap of 100 bp

36687 36786: gap of 100 bp

36687 37516: contig of 730 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10467 10566: gap of 100 bp
10567 11291: contig of 725 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7297 8013: contig of 717 bp in length

8014 8113: gap of 100 bp

8114 8242: contig of 711 bp in length

8825 8924: gap of 100 bp

8925 9649: contig of 725 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21970 22069; gap of 100 bp 22070 22774; contig of 705 bp in length 22075 22874; gap of 100 bp 22975 23595; contig of 721 bp in length 23596 23695; gap of 100 bp 24428; contig of 733 bp in length 23696 24428; contig of 733 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100 bp
12334 12233; gap of 100 bp
12915; contig of 682 bp in length
12916 13015; gap of 100 bp
13016 13762; contig of 747 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24428: contig of 733 bp in length 24528: gap of 100 bp 1 25348: contig of 720 bp in length 1 25348: gap of 100 bp 1 2548: contig of 720 bp in length 1 2548: contig of 720 bp in length 1 2548: gap of 100 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               391: gap of 100 bp
12133: contig of 742 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 162: gap of 100 bp
14587: contig of 725 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9: gap of 1
10466: contig of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BASE COUNT
                                                                                                                                                                                                    RESULT 10
AC096120
                                                                                                                                                                                                                                                                                                                                  밁
                                                                                                                                     DEFINITION
                                      VERSION
                                                                      ACCESSION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23787 ATTTCTAGGGTCTTTGTTCTAGTTGAGCTTTTCATTGTTAAGGTCTAAAATCTTGTCACA 23846
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23727 TCCTCTGCCATCCCAGAGAGATGACCACGTCAATTCCCAGAGGTGACACCACTCTGAGTCC 23786
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23847
                                                                                                                                                                                                                                                                                                                                      23967 GGGAAGGAAAAAATA 23981
                                                                                                                                                                                                                                                                                                                                                                                                                                                             23907 GTTCAGAATTCAGTTGAAAAAGTTACCCAGGATGAGTTCCTATGTTTGACTTGAAGA 23966
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           310 TTCTCTGTGGTCCCAAAGAGATGACCATATTGACTGTAGAAATCACACCACCATAAAAGC 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         370 CCATCTGGGGAGCCATTTCCAGACTGATCTTTTTATCATTAAGGTTTGAATTCTTGCCACG 429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                490 TGTTCAGAATTCAGTGGGCTTGGTCAGCTAATGGAAATGATCTATGGTTTGACTTAAATG 549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              430 TGTGGGTTTTAAGGTTTTTAGGGATTTTTATCTAGCGGCACTCACCTGCTTCCCTGTGAA 489
                                                                                                                                                                                                                                                                                                                                                                                                     550 TGAAAGGAAAAAAA 564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TGGAGTTTTTAAGATTTTTAGGGATGTCTATTAAGAAAAGCATGGCTGCTTTTCCCAACT 23906
                                                           102783 bp D
Rattus norvegicus clone CH230-11B19,
***, 51 unordered pieces.
AC096120
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43216 43315; gap of 100 bp
43216 43315; gap of 100 bp
44028; contig of 713 bp in length
44129 44128; gap of 100 bp
44129 44814; contig of 686 bp in length
44121 44914; gap of 100 bp
44915 45485; contig of 571 bp in length
45486 45585; gap of 100 bp
46312 46411; gap of 100 bp
46412 47158; contig of 726 bp in length
46412 47158; contig of 747 bp in length
47159 48001; contig of 747 bp in length
48002 48101; gap of 100 bp
48002 48101; gap of 100 bp
48003 4857; contig of 756 bp in length
48104 4857; contig of 756 bp in length
48105 4857; contig of 768 bp in length
4858 48957; gap of 100 bp
48658; contig of 708 bp in length
4858 48957; gap of 100 bp
48658; contig of 708 bp in length
                                      AC096120.3 GI:17943804
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11307 a 10320 c 10885 g 11020 t 6133
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37617 38346: contig of 730 bp in length
38347 38446: gap of 100 bp
38447 39150: contig of 704 bp in length
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40014 40761: contid of 740
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/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone="RP11-615H7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .49665
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4.7%; Score ... 3.7e-12; 56.5%; Pred. No. 3.7e-12; Indels rative 0; Mismatches 111; Indels
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42399: contig of 693 bp
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41606: contig of 745 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    p of 100 bp
contig of 748 bp in length
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Pred. No. 3.7e-12;
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*** SEQUENCING IN PROGRESS
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JOURNAL
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AUTHORS
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TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Carter, M., Burkett, C., Burrell, K.L., Byda, N.C., Charco, T.F., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D., Chen, G., Chen, G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Direct Submission

Submitted (17-SEP-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

On Dec 20, 2001 this sequence version replaced gi:16901736.
                                                                                                                                                                                                                                                                                                                                                                   findPhrapList
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished
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Rattus norvegicus
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Mammalla; Eutheria; Rodentla; Sciurognathi; Muridae; Murinae;
                                                                                             Consensus quality: 92140 bases at least Q40 Consensus quality: 98027 bases at least Q30 Consensus quality: 102801 bases at least Q20 Estimated insert size: 79332; sum-of-contigs estimation
Quality coverage: 0x in Q20 bases; agarose-fp estimation Quality coverage: 1x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                          Assembly program: Phrap; version 0.990329First call to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Center clone name: CH230-11B19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Center project name: GEMB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Web site: http://www.hgsc.bcm.tmc.edu/Contact: hgsc-help@bcm.tmc.edu
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* NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

* NOTE: This is a 'working draft' sequence. It currently consists of 51 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;

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FEATURES
          SOURCE
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                              VERSION
                                                                                    AC095179/c
                    KEYWORDS
                                           ACCESSION
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Best Local Similarity
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ORGANISM
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                                                                                                                                                                                                                                            345 GTAGAAATCACACCACCATAAAAGCCCCATCTGGGAGCC 382
                                              171322 bp DNA linear HTG 20-DEC-2001 Rattus norvegicus clone CH230-9C13, *** SEQUENCING IN PROGRESS ***, 64 unordered pieces.
Rattus norvegicus
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           Norway rat.
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/db_xref="taxon:10116"
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100542: contig of 1168 b
100642: gap of unknown l
101651: contig of 1009 b
101751: gap of unknown l
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Direct Submission
Submitted (16-SEP-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA On Dec 20, 2001 this sequence version replaced gi:15625733.
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* NOTE: Estimated insert size may differ from sequence length 
* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html) 
* NOTE: This is a 'working draft' sequence. It currently
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                                                                                                                                                             Consensus quality: 147096 bases at least Q40 Consensus quality: 154402 bases at least Q30 Consensus quality: 160566 bases at least Q20 Estimated insert size: 145980; sum-of-contigs estimation Quality coverage: 0x in Q20 bases; agarose-fp estimation Quality coverage: 2.3x in Q20 bases; sum-of-contigs estimation
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Assembly program: Phrap; version 0.990329First call to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Center clone name: CH230-9C13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: hgsc-help@bcm.tmc.edu
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consists of 64 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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Submitted (23-NOV-2001) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
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Birren,B., Linton,L., Nusbaum,C. and Lander,E.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sequencing reads that have not been assembled into contigs. Runs of N are used to separate the reads and the order in which they appear is completely arbitrary. Low-pass sequence sampling is useful for identifying clones that may be gene-rich and allows overlap relationships among clones to be deduced. However, it should not be assumed that this clone will be sequenced to completion. In the event that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 the record
be preserve
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647 2374: contig of 728 bp in length
375 2474: gap of 100 bp
75 3195: contig of 721 bp in length
96 3295: gap of 100 bp
96 3295: gap of 100 bp
16 4033: contig of 721 bp in length
                                       100 bp 1 length 6520: contig of 726 bp in length 7350: contin of 7250 bp 7450
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1546: contig of 718 bp in length
1646: gap of 100 bp
1646: gap of 728 bp in length
                7450:
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4966: gap of 100 bp
5694: contig of 728 bp in length
794: gap of 100 bp
6520: contig of 728 contig of 728 bp in length
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16382: contig of 730 bp in length
16383 16482: gap of 100 bp
16483 17201: contig of 719 bp in length
17202 17301: gap of 100 bp
17302 18013: contig of 712 bp in length
18014 18113: gap of 100 bp
18114 18826: contig of 713 bp in length
18827 18926: gap of 100 bp
19649 19748: gap of 100 bp
19649 19748: gap of 100 bp
19749 20770: contig of 722 bp in length
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35131: contig of 724 bp
5231: gap of 100 bp
35958: contig of 727 bp
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26207: contig of 712 bp
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                                                                                                                                                                                                                   1 4.3%; Score 72.2; DB 2; Length 72930; Similarity 40.2%; Pred. No. 1.5e-10;
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48396 49105; contig of 710 bp in length
49106 49205; gap of 100 bp
49206 49927; contig of 722 bp in length
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56478: contig of 711 bp in length
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55667: contig of 717 bp in length
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48295: contig of 703 bp in length
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45852: contig of 714 bp in length
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45038: contig of 714 bp in length
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Lee,C.-M. and Chang,Y.-S.
Direct Submission
                      Benton, J., Bimage, K., Blankenburg, K., Bonnin, D., Bouck, J., Bowie, S., Brieva, M., Brown, E., Brown, B., Bryant, N. P., Bunday, C., Burch, P., Burkett, C., Burrell, K. L., Byrd, N. C., Carron, T. F., Carter, M., Cavazos, S. R., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C., Cleveland, C. D., Cox, C., Coyle, M. D., Dathorne, S. R., David, R., David, M. L., Davis, C., Davy, Carroll, L., Dederich, D. A., Delaney, K. R., Delgado, O., Denn, A. L., Ding, Y., Dinh, H. H., Douthwaite, K. J., Draper, H., Denn, A. L., Ding, Y., Dinh, H. H., Douthwaite, K. J., Draper, H., Delgado, O., Denn, A. L., Ding, Y., Dinh, H. H., Douthwaite, K. J., Draper, H., Delgado, O., Denn, A. L., Ding, Y., Dinh, H. H., Douthwaite, K. J., Draper, H., Delgado, O., 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (06-SEP-2001) Graduate Institute of Basic Medical Sciences, Chang-Gun University School of Medicine, 259 Wen-Road, Kwei-Shan, Tao-Yuan, Taiwan 033, Republic of China
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rattus norvegicus clone CH230-189013, *** SEQUENCING IN PROGRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lee, C.-M. and Chang, Y.-S. 129/SvJ mouse genomic clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa;
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                                                                                                                                                                                                                                                                                                                 Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C., Alsbrooks,S.L., Amaratunge,H.C., Are,J.R., Banks,T., Barbaria,J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rattus norvegicus
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Dugan-Rocha, S., Durbin, K.J., Earnhart, C., Edgar, D., Edwards, C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Norway rat
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                                                                                                                                                                                                                                                                                                                                                                                                (bases 1 to 176047)
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/chromosome="6"
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Elhaj.C., Escotto,M., Falls,T., Ferraguto,D., Flagg,N., Ford,J., Garcar,P., Frantz,P., Gabisi,A., Gao,J., Garcia,A., Garner,T., Garza,N., Gill,R., Gorrell,J.H., Guevara,W., Gunaratne,P., Hale,S., Hamilton,K., Harris,C., Harris,K., Harth,M., Havlak,P., Hawes,A., Hollows,C., Harris,K., Harth,M., Holloway,C., Hollins,B., Homsi,F., Howard,S., Huber,J., Holloway,C., Jackson,L.E., Jacobson,B., Jia,Y., Johnson,R., Jolivet,S., Joudah,S., Karlsson,E., Kelly,S., Khan,U., King,L., Korvah,J., Kovar,C., Kratovic,J., Kureshi,A., Landry,N., Leal,B., Lewis,L., Li,J., Li,Z., Lichtarge,O., Lieu,C., Liu,J., Liu,W., Loulseged,H., Lozado,R.J., Lu,X., Lucier,A., Lucier,R., Luna,R., Martinez,E., Massey,E., Martiney,E., Martindale,A., Martinez,E., Massey,E., Mawhiney,E., McLeod,M.P., Meador,M., Morgan,M., Morris,S., Moser,M., Neal,D., Newtson,J., Newtson,N., Nguyen,A., Nguyen,N., Nickerson,E., Nwokenkwo,S., Oguh,M., Okwuon,G., Oragunye,N., Oviedo,R., Pace,A., Payton,B., Peery,J., Perez,L., Peters,L., Pickens,R., Primus,E., Pu,L.L., Ouiles,M., Ren,Y., Rives,M., Rojas,A., Rojubokan,I., Rolfe,M., Ruiz,S., Savery,G., Scherer,S., Scott,G., Shen,H., Stone,H., Sutton,A., Svatek,A., Tabor,P., Tamerisa,A., Tamerisa,K., Tang,H., Tansey,J., Taylor,C., Taylor,T., Telfrod,B., Thomas,N., Thomas,S., Walliams,G., Walliamson,A., Waezyk,R., Wooden,S., Walliams,G., Williamson,A., Waezyk,R., Wooden,S., Walliams,G., Williamson,A., Waezyk,R., Wooden,S., Welsen,C., Wu,Y., Wu,Y.F., Zhou,J., Zorrilla,S., Nelson,D., Vincer, Suhmission, R., Welsen,R., Wooden,S., Welsen,R., Wooden,S., Welsen,R., Wooden,S., Welsen,R., Wooden,S., Welsen,R., Wooden,S., Welsen,R., Wooden,S., Walliamson,A., Wiezyk,R., Wooden,S., Welsen,R., Wooden,S., Welsen,R., Wooden,S., Welsen,R., Wooden,S., Welsen,R., Wooden,S., Welsen,R., Wooden,S., Wooden,S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (09 NOV-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      findPhrapList
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On Dec 21,
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                                                                                                                                                                                                                                                                                                                                                                        (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

NOTE: This is a 'working draft' sequence. It currently consists of 42 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence
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                                                                                                                                                                                                                                                                                                               be preserved
                                                                                                                                                                                                                                                                                                                                                            as soon as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Consensus quality: 151055 bases at least Q40 Consensus quality: 158732 bases at least Q30 Consensus quality: 165129 bases at least Q30 Estimated insert size: 160905; sum-of-contigs estimation Quality coverage: 0x in Q20 bases; agarose-fp estimation quality coverage: 2.5x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Center clone name: CH230-189013
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: hgsc-help@bcm.tmc.edu
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                                        12798: contig of 12798 bp in length 12898: gap of unknown length 25227: contig of 12329 bp in length 25327: gap of unknown length 37905: contig of 12578 bp in length 45387: contig of 7382 bp in length 45387: contig of 7382 bp in length
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                                                                                                                                                                 Burch, P., Burkett, C., Burcwin, E., Browin, M., Byrdin, N. F., Bundy, C.,
Burcch, P., Burkett, C., Burrell, K.L., Byrd, N.C., Carron, T. F.,
Carter, M., Cavazos, S.R., Chacko, J., Chavez, D., Chen, G., Chen, R.,
Chen, Z., Chowdhry, I., Christopoulos, C., Cleveland, C.D., Cox, C.,
Coyle, M.D., Dathorne, S.R., David, R., David, M.L., Davis, C.,
Davy, Carroll, L., Dederich, D.A., Delaney, K.R., Delgado, O.,
Davy, Carroll, L., Dederich, D.A., Delaney, K.R., Delgado, O.,
Davy, Carroll, L., Dederich, D.A., Delaney, K.R., Delgado, O.,
Davy, Carroll, L., Doderich, D.A., Delaney, K.R., Delgado, O.,
Davy, Carroll, L., Doderich, D.A., Delaney, K.R., Delgado, O.,
Davy, Carroll, L., Douthwaite, K.J., Draper, H.,
Denn, A.L., Ding, Y., Dinh, H.H., Douthwaite, K.J., Draper, H.,
Denn, A.L., Ding, Y., Dinh, H.H., Douthwaite, K.J., Draper, H.,
Denn, A.L., Ding, Y., Dinh, H.H., Douthwaite, K.J., Draper, H.,
Denn, A.L., Ding, Y., Dinh, H.H., Douthwaite, K.J., Draper, H.,
Denn, A.L., Ding, Y., Dahh, H.H., Douthwaite, K.J., Draper, H.,
Bernandez, J., Haris, T., Ferraguto, D., Flagg, N., Ford, J.,
Hanilton, K., Harris, C., Harris, K., Hart, M., Havlak, P., Hawes, A.,
Hernandez, J., Hernandez, O., Hodgson, A., Hogues, M., Holloway, C.,
Heanilton, K., Harris, C., Harris, K., Hart, M., Havlak, P., Hawes, A.,
Jackson, L.E., Jacobson, B., Jia, Y., Johnson, R., Jolivet, S.,
Jackson, L., Li, J., Li, Z., Lichtarge, O., Lieu, C., King, L., Korvah, J.,
Kovar, C., Kratovic, J., Kureshi, A., Landry, N., Leal, B., Lewis, L.C.,
Lewis, L.C., Kratovic, J., Kureshi, A., Landry, N., Leal, B., Lewis, L.C.,
Ma, J., Maheshwari, M., Mapua, P., Martin, R., Martindale, A.,
Martinez, E., Massey, E., Mawhiney, E., McLeod, M.P., Meador, M.,
Martinez, E., Massey, E., Mawhiney, E., McLeod, M.P., Meador, M.,
Martinez, E., Massey, E., Mawhiney, E., McLeod, M.P., Meador, M.,
Martinez, E., Massey, E., Mawhiney, E., Pull, L.,
Mei, G., Metzker, M., Miner, G., Miner, Z., Mitchell, T., Wohabbat, K.,
Majusen, L., Savery, G., Scherer, S., Scott, G., Shen, H., Shooshtari, 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-Osman,F.R., Allen,C., Alsbrooks,S.L., Amaratunge,H.C., Are,J.R., Banks,T., Barbaria,J., Benton,J., Bimage,K., Blankenburg,K., Bonnin,D., Bouck,J., Bowie,S., Brieva,M., Brown,E., Brown,M., Brant,N.P., Buhay,C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    184550 bp DNA linear HTG 20-DEC-201
Rattus norvegicus clone CH230-8E8, *** SEQUENCING IN PROGRESS ***
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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Sisson,I., Sodergren,E., Sonaike,T., Sparks,A., Stanley,H., Stone,H., Sutton,A., Svatck,A., Tabor,P., Tamerisa,A., Tamerisa,A., Tangy,H., Tansey,J., Taylor,C., Taylor,T., Telfrod,B., Thomas,N., Thomas,S., Usmani,K., Vasquez,L., Vera,V., Villalon,D., Vinson,F wall,R., Wang,S., Ward-Moore,S., Warren,R., Washington,C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              51505 a
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                                                                                                                              Tamerisa, K.
                                                       Vinson, R.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (17-SEP-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA On Dec 20, 2001 this sequence version replaced gi:15627273.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Direct
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            * NOTE: Estimated insert size may differ from sequence length
(see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

* NOTE: This is a 'working draft' sequence. It currently

* consists of 59 contigs. The true order of the pieces

* is not known and their order in this sequence record is

* arbitrary. Gaps between the contigs are represented as

* runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  be preserved
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 as soon as it is available and the accession number will
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
----- Project Information
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Assembly program: Phrap; version 0.990329First call to
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